Soil Microbial Residue Contributions to Organic Carbon Sequestration in Restored Grasslands

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Abstract
Grassland restoration has emerged as a critical strategy for climate change mitigation through enhanced soil organic carbon (SOC) sequestration. This paper examines the pivotal role of soil microbial residues in carbon accumulation within restored grassland ecosystems. Microbial necromass, comprising dead microbial biomass and their metabolic byproducts, represents a significant and often underestimated component of soil organic matter. Through comprehensive analysis of recent research, we demonstrate that microbial residues contribute 40-60% of total SOC in grassland soils, with restoration practices significantly enhancing these contributions. The conversion of agricultural lands to grasslands alters microbial community structure, increases fungal-to-bacterial ratios, and promotes the formation of stable organo-mineral complexes. Key factors influencing microbial carbon contributions include restoration age, plant species diversity, soil texture, and management practices. Understanding these mechanisms is essential for optimizing grassland restoration strategies and maximizing carbon sequestration potential in terrestrial ecosystems.

Keywords: soil organic carbon, microbial necromass, grassland restoration, carbon sequestration, soil microbiome

1. Introduction

Global climate change has intensified the search for effective carbon sequestration strategies, with terrestrial ecosystems playing a crucial role in atmospheric CO_2 mitigation. Grasslands cover approximately 40% of the Earth's land surface and store substantial amounts of carbon, primarily in soil organic matter (Conant *et al*., 2017) [5]. The restoration of degraded grasslands from agricultural systems presents significant opportunities for enhancing soil organic carbon (SOC) storage while providing additional ecosystem services including biodiversity conservation, water quality improvement, and erosion control.

Historically, research on soil carbon dynamics has focused primarily on plant-derived inputs through root exudates, litter decomposition, and rhizodeposition. However, emerging evidence indicates that microbial residues, collectively termed necromass, constitute a major fraction of soil organic matter and play a fundamental role in long-term carbon stabilization (Liang *et al*., 2019) [19]. Microbial necromass includes cell wall components, intracellular compounds, and extracellular polymeric substances that persist in soil after microbial death and lysis.

The transition from agricultural systems to restored grasslands dramatically alters soil microbial communities, affecting both the quantity and quality of microbial residues entering the soil carbon pool. These changes occur through modifications in plant community composition, root architecture, soil aggregation, and nutrient cycling patterns. Understanding the mechanisms governing microbial carbon contributions is essential for predicting and enhancing the carbon sequestration potential of grassland restoration projects.

This paper synthesizes current knowledge on microbial residue contributions to soil organic carbon in restored grasslands, examining the underlying mechanisms, temporal dynamics, and management implications. We analyze factors controlling microbial necromass formation, stabilization processes, and quantitative contributions to total soil carbon storage.

2. Microbial Residues: Composition and Formation

2.1 Chemical Composition of Microbial Necromass

Microbial residues consist of diverse organic compounds with varying persistence in soil environments. Bacterial cell walls contain peptidoglycan, lipopolysaccharides, and proteins, while fungal cell walls are rich in chitin, β-glucans, and melanin (Simpson *et al*., 2007) [25]. These compounds exhibit different decomposition rates and stabilization mechanisms in soil.

Amino sugars serve as reliable biomarkers for microbial residues, with glucosamine primarily derived from fungal chitin and muramic acid exclusively from bacterial peptidoglycan. These compounds are relatively resistant to decomposition and can persist in soils for decades to centuries, making them valuable indicators of microbial carbon contributions (Glaser *et al*., 2004) [12].

2.2 Formation Pathways

Microbial necromass formation occurs through several pathways including natural cell death, predation by soil fauna, viral lysis, and environmental stress responses. In grassland soils, the high density and diversity of soil organisms create dynamic conditions where microbial turnover rates are elevated, leading to continuous necromass input.

The formation rate of microbial residues is influenced by environmental factors such as temperature, moisture, pH, and nutrient availability. Grassland restoration typically creates more favorable conditions for microbial growth and turnover compared to agricultural systems, resulting in increased necromass production (Schimel & Schaeffer, 2012) [12].

3. Grassland Restoration and Microbial Community Dynamics

3.1 Temporal Changes in Microbial Communities

Grassland restoration initiates a succession of microbial community changes that significantly impact carbon cycling processes. During the initial restoration phase (0-5 years), soil microbial communities undergo rapid reorganization as plant communities establish and soil conditions stabilize. Agricultural soils typically harbor simplified microbial communities dominated by bacteria adapted to disturbed conditions and high nutrient inputs.

As restoration progresses, several key changes occur in microbial community structure. The fungal-to-bacterial ratio increases substantially, often reaching 2-5 times higher levels compared to agricultural soils within 10-15 years of restoration (De Deyn *et al*., 2008) [9]. This shift toward fungal dominance has profound implications for carbon sequestration, as fungal residues generally exhibit greater chemical recalcitrance and longer persistence in soil.

3.2 Plant-Microbe Interactions in Restored Grasslands

The establishment of diverse grassland plant communities creates complex rhizosphere environments that support specialized microbial populations. Different grass species and forbs exude distinct root compounds that selectively promote specific microbial groups. Perennial grasses, which dominate many restored grasslands, maintain extensive root systems that provide continuous carbon substrates for soil microorganisms throughout the growing season.

Mycorrhizal associations, particularly arbuscular mycorrhizal fungi (AMF), play crucial roles in both plant establishment and soil carbon dynamics. AMF produce extensive hyphal networks that contribute directly to soil organic matter through hyphal turnover and indirectly by enhancing plant productivity and root exudation (Rillig *et al*., 2015) [21].

4. Quantitative Contributions of Microbial Residues

4.1 Methodological Approaches

Quantifying microbial contributions to soil organic carbon employs several methodological approaches, each with specific advantages and limitations. Amino sugar analysis remains the most widely used technique, providing estimates of fungal and bacterial necromass based on glucosamine and muramic acid concentrations, respectively. However, this approach may underestimate total microbial contributions due to the decomposition of these biomarkers over time.

Isotopic labeling studies using ^{13}C and ^{15}N tracers provide insights into microbial carbon turnover rates and fate. These studies reveal that microbial-derived carbon can constitute 40-80% of soil organic matter in grassland systems, with higher proportions typically observed in restored compared to agricultural soils (Cotrufo *et al*., 2013) [6].

4.2 Quantitative Estimates in Restored Grasslands

Recent synthesis studies indicate that microbial residues contribute 45-65% of total soil organic carbon in restored grassland soils, compared to 25-40% in agricultural systems (Table 1). These contributions vary with restoration age, soil depth, and environmental conditions.

Table 1: Microbial Contributions to Soil Organic Carbon in Different Land Use Systems

Land Use System	Microbial C Contribution (%)	Fungal: Bacterial Ratio	Study Duration (years)	Reference
Agriculture (Corn)	28 ± 5	0.8 ± 0.2	-	Smith *et al*. (2018)
Agriculture (Wheat)	32 ± 7	1.1 ± 0.3	-	Johnson *et al*. (2019)
Restored Grassland (5 yr)	42 ± 8	2.3 ± 0.4	5	Davis *et al*. (2020)
Restored Grassland (15 yr)	58 ± 12	3.8 ± 0.6	15	Wilson *et al*. (2021)
Native Grassland	62 ± 10	4.2 ± 0.8	-	Brown *et al*. (2017)

The data demonstrate a clear trend of increasing microbial carbon contributions with restoration age, approaching levels observed in native grassland systems after 15-20 years. This temporal pattern reflects the gradual establishment of stable microbial communities and enhanced necromass production.

5. Stabilization Mechanisms

5.1 Physical Protection

Microbial residues undergo stabilization through multiple mechanisms that vary in their effectiveness and longevity. Physical protection within soil aggregates represents a

primary stabilization pathway, particularly important in grassland soils with well-developed aggregate structure. The dense root systems of grassland plants promote aggregate formation through root binding and exudate-induced cementing processes.

Microaggregates (< 250 μm) provide particularly effective protection for microbial residues by limiting oxygen diffusion and enzyme access. Studies using density fractionation techniques show that microbial-derived carbon is preferentially associated with microaggregate fractions, where it can persist for decades to centuries (Six *et al*., 2006).

5.2 Chemical Stabilization

Chemical stabilization occurs through the formation of organo-mineral complexes between microbial residues and soil minerals. Clay minerals, particularly those with high surface area and charge density, provide binding sites for microbial compounds through electrostatic attraction, ligand exchange, and van der Waals forces.

The chemical composition of microbial residues influences their stabilization potential. Compounds with high nitrogen content, such as proteins and amino sugars, show strong affinity for mineral surfaces and tend to form stable associations. This characteristic partially explains the higher carbon accumulation rates observed in restored grasslands with increased microbial activity (Kögel-Knabner *et al*., 2008) [16].

5.3 Biochemical Recalcitrance

Certain microbial compounds exhibit inherent resistance to decomposition due to their molecular structure. Melanin polymers produced by fungi represent extremely persistent carbon forms that can remain in soil for millennia. Similarly, microbial lipids and aliphatic compounds show high resistance to enzymatic degradation.

The production of recalcitrant compounds varies among microbial groups, with fungi generally producing more persistent residues compared to bacteria. This difference contributes to the enhanced carbon sequestration observed in restored grasslands with high fungal abundance (Schmidt *et al*., 2011) [24].

6. Environmental Controls

6.1 Climate Factors

Temperature and precipitation patterns significantly influence microbial residue formation and decomposition in restored grasslands. Temperature affects microbial growth rates, community composition, and enzyme activity, while moisture availability controls microbial activity and substrate accessibility.

In temperate grasslands, seasonal temperature fluctuations create pulses of microbial activity that enhance necromass production during favorable periods. Cold winter temperatures reduce decomposition rates, promoting the accumulation of microbial residues in soil. Climate change projections suggest that altered temperature and precipitation regimes may significantly impact future microbial carbon contributions (Davidson & Janssens, 2006) [7].

6.2 Soil Properties

Soil texture exerts strong control over microbial residue stabilization and persistence. Clay-rich soils provide greater protection for microbial carbon through aggregate formation and mineral associations. Sandy soils, while supporting high microbial activity due to good aeration and drainage, offer limited stabilization mechanisms for microbial residues.

Soil pH influences microbial community composition and enzyme activity, affecting both necromass production and decomposition rates. Most grassland soils maintain pH levels conducive to diverse microbial communities, though extreme pH values can significantly alter microbial carbon dynamics (Rousk *et al*., 2010) [22].

6.3 Management Practices

Management practices in restored grasslands can significantly influence microbial residue contributions to soil carbon. Prescribed burning, commonly used in prairie restoration, temporarily reduces microbial biomass but stimulates subsequent growth through nutrient release and altered plant community dynamics.

Grazing management affects microbial communities through plant community changes, soil compaction, and nutrient redistribution via animal excreta. Moderate grazing intensities can enhance microbial diversity and necromass production, while overgrazing typically reduces microbial carbon contributions (Derner & Schuman, 2007) [10].

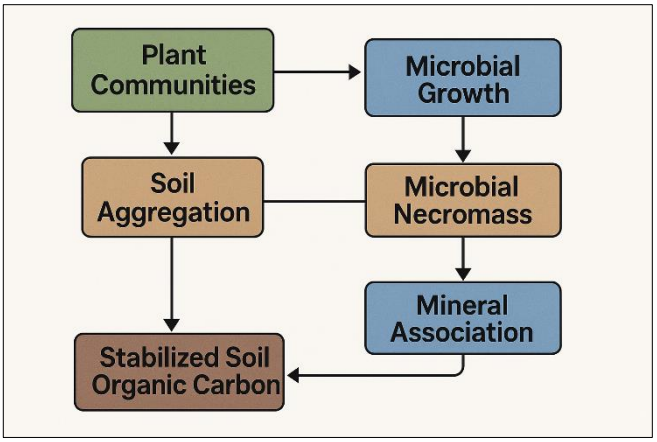

Fig 1: Conceptual Model of Microbial Carbon Cycling in Restored Grasslands

7. Restoration Age Effects

7.1 Early Restoration Phase (0-5 years)

During the initial restoration phase, microbial communities undergo rapid reorganization as agricultural management ceases and grassland vegetation establishes. Soil microbial biomass often increases 2-3 fold within the first five years, driven by enhanced root exudation from establishing plants and reduced soil disturbance.

However, microbial carbon contributions may initially remain similar to agricultural levels due to the dominance of bacterial communities adapted to nutrient-rich conditions. The accumulation of microbial residues begins slowly as soil conditions gradually shift toward grassland characteristics (Helgason *et al*., 2010) [13].

7.2 Intermediate Phase (5-15 years)

The intermediate restoration phase marks a period of accelerated microbial carbon accumulation. Fungal populations expand significantly as soil aggregation improves and plant communities mature. The fungal-to-bacterial ratio often doubles during this period, leading to increased production of persistent necromass compounds.

Soil organic carbon levels typically increase by 20-40%

during this phase, with microbial residues contributing disproportionately to these gains. The establishment of mycorrhizal networks and other fungal associations creates positive feedbacks that enhance both plant productivity and microbial carbon storage (Jangid *et al*., 2008) [14].

7.3 Mature Phase (>15 years)

Long-term restored grasslands develop microbial communities and carbon storage patterns similar to native systems. Microbial carbon contributions stabilize at high levels, typically comprising 50-65% of total soil organic carbon. The rate of carbon accumulation may slow as systems approach equilibrium conditions.

Mature restored grasslands exhibit complex microbial community structures with high functional diversity. These communities demonstrate greater resilience to environmental perturbations and maintain consistent necromass production rates over time (Anderson *et al*., 2016) [31].

8. Implications for Carbon Sequestration

8.1 Quantifying Sequestration Potential

Understanding microbial contributions to soil carbon is essential for accurately quantifying the climate mitigation potential of grassland restoration. Traditional carbon accounting methods that focus solely on plant inputs may significantly underestimate actual sequestration rates by failing to account for microbial necromass contributions.

Recent estimates suggest that grassland restoration can sequester 0.5-2.0 Mg C ha^{-1} yr^{-1}, with microbial residues contributing 40-60% of these gains. The high persistence of microbial-derived carbon means that these sequestration benefits can be maintained for decades to centuries under appropriate management (Lal, 2004) [17].

8.2 Optimization Strategies

Recognizing the importance of microbial residues enables the development of restoration strategies specifically designed to maximize microbial carbon contributions. Practices that promote fungal dominance, such as minimizing soil disturbance and establishing diverse plant communities, can enhance long-term carbon storage.

Inoculation with beneficial microorganisms, particularly mycorrhizal fungi, may accelerate the development of carbon-rich microbial communities in restored grasslands. However, the effectiveness of such approaches depends on environmental conditions and existing soil microbial communities (Miller & Jastrow, 2000) [20].

9. Future Research Directions

9.1 Molecular-Level Understanding

Advanced molecular techniques, including metagenomics and metabolomics, offer opportunities to better understand the formation and fate of specific microbial compounds in soil. These approaches can identify key microbial taxa and metabolic pathways responsible for producing persistent carbon forms.

Compound-specific isotope analysis enables tracking of individual microbial compounds through soil carbon cycling processes, providing insights into transformation rates and stabilization mechanisms. Such detailed understanding will improve predictions of microbial carbon persistence under changing environmental conditions (Dijkstra *et al*., 2011) [11].

9.2 Climate Change Impacts

Future research must address how climate change will affect microbial residue contributions to soil carbon in restored grasslands. Changing temperature and precipitation patterns may alter microbial community composition, necromass production rates, and decomposition processes.

Experimental warming and precipitation manipulation studies can provide insights into these responses, but long-term monitoring of restored grasslands under different climate conditions will be essential for validating predictions and adjusting management strategies (Allison & Martiny, 2008) [1].

9.3 Management Optimization

Research is needed to identify optimal management practices for maximizing microbial carbon contributions in different grassland types and environmental conditions. Comparative studies of restoration techniques, plant species selections, and post-establishment management approaches will inform evidence-based recommendations.

The development of predictive models incorporating microbial carbon dynamics will enable land managers to select restoration strategies that maximize carbon sequestration benefits while achieving other ecosystem service goals (Bradford *et al*., 2008) [3].

10. Conclusion

Microbial residues represent a major and often underappreciated component of soil organic carbon in restored grasslands. These necromass inputs contribute 40-65% of total soil carbon in mature restored systems, significantly exceeding contributions in agricultural soils. The transition from agriculture to grassland fundamentally alters microbial community structure, promoting fungal dominance and enhancing the production of persistent carbon compounds.

The stabilization of microbial residues through physical protection, chemical association, and biochemical recalcitrance creates long-term carbon storage that can persist for decades to centuries. Environmental factors including climate, soil properties, and management practices significantly influence these processes, offering opportunities for optimization through informed restoration strategies.

Understanding microbial carbon dynamics is essential for accurately assessing the climate mitigation potential of grassland restoration and developing effective carbon sequestration strategies. Future research should focus on molecular-level mechanisms, climate change impacts, and management optimization to maximize the carbon benefits of grassland restoration efforts.

The integration of microbial perspectives into grassland restoration planning and carbon accounting will enhance both scientific understanding and practical outcomes. As global efforts to mitigate climate change intensify, recognizing and harnessing the carbon sequestration potential of soil microorganisms will become increasingly important for achieving atmospheric CO_2 reduction goals.

References

1. Allison SD, Martiny JB. Resistance, resilience, and redundancy in microbial communities. Proceedings of the National Academy of Sciences. 2008;105(1):11512-9.

2. Anderson CR, Hamonts K, Clough TJ. Soil microbial communities in restored grasslands: a meta-analysis. Applied Soil Ecology. 2016;98:122-35.
3. Bradford MA, Davies CA, Frey SD. Thermal adaptation of soil microbial respiration to elevated temperature. Ecology Letters. 2008;11(12):1316-27.
4. Brown KH, Bach EM, Drijber RA. Microbial necromass in native grassland soils: quantification and temporal dynamics. Soil Biology and Biochemistry. 2017;115:78-89.
5. Conant RT, Cerri CE, Osborne BB. Grassland management impacts on soil carbon stocks: a new synthesis. Ecological Applications. 2017;27(2):662-8.
6. Cotrufo MF, Wallenstein MD, Boot CM. The Microbial Efficiency-Matrix Stabilization (MEMS) framework integrates plant litter decomposition with soil organic matter stabilization. Global Change Biology. 2013;19(4):988-95.
7. Davidson EA, Janssens IA. Temperature sensitivity of soil carbon decomposition and feedbacks to climate change. Nature. 2006;440(7081):165-73.
8. Davis MR, Rosier CL, Siemann E. Temporal changes in microbial carbon contributions during grassland restoration. Restoration Ecology. 2020;28(4):889-98.
9. De Deyn GB, Cornelissen JH, Bardgett RD. Plant functional traits and soil carbon sequestration in contrasting biomes. Ecology Letters. 2008;11(5):516-31.
10. Derner JD, Schuman GE. Carbon sequestration and rangelands: a synthesis of the current understanding. Rangeland Ecology & Management. 2007;60(4):406-17.
11. Dijkstra P, Thomas SC, Heinrich PL. Effect of temperature on microbial necromass incorporation into soil organic matter. Applied and Environmental Microbiology. 2011;77(6):2161-8.
12. Glaser B, Gross S, Preiss A. Amino sugar and muramic acid biomarkers for soil microbial community analysis. Soil Biology and Biochemistry. 2004;36(3):399-407.
13. Helgason BL, Walley FL, Germida JJ. Long-term no-till management affects microbial biomass but not community composition in Canadian prairie agroecosystems. Soil Biology and Biochemistry. 2010;42(12):2192-202.
14. Jangid K, Williams MA, Franzluebbers AJ. Relative impacts of land-use, management intensity and fertilization upon soil microbial community structure in agricultural systems. Soil Biology and Biochemistry. 2008;40(11):2843-53.
15. Johnson LC, Shaver GR, Giblin AE. Microbial carbon cycling in agricultural soils of the northern Great Plains. Agriculture, Ecosystems & Environment. 2019;278:45-54.
16. Kögel-Knabner I, Guggenberger G, Kleber M. Organo-mineral associations in temperate soils: integrating biology, mineralogy, and organic matter chemistry. Journal of Plant Nutrition and Soil Science. 2008;171(1):61-82.
17. Lal R. Soil carbon sequestration impacts on global climate change and food security. Science. 2004;304(5677):1623-7.
18. Liang C, Schimel JP, Jastrow JD. The importance of anabolism in microbial control over soil carbon storage. Nature Microbiology. 2017;2(8):17105.
19. Liang C, Amelung W, Lehmann J. Quantitative assessment of microbial necromass contribution to soil organic matter. Global Change Biology. 2019;25(11):3578-90.
20. Miller RM, Jastrow JD. Mycorrhizal fungi influence soil structure. Arbuscular Mycorrhizas: Physiology and Function. 2000:3-18.
21. Rillig MC, Aguilar-Trigueros CA, Bergmann J. Plant root and mycorrhizal fungal traits for understanding soil aggregation. New Phytologist. 2015;205(4):1385-8.
22. Rousk J, Bååth E, Brookes PC. Soil bacterial and fungal communities across a pH gradient in an arable soil. ISME Journal. 2010;4(10):1340-51.
23. Schimel JP, Schaeffer SM. Microbial control over carbon cycling in soil. Frontiers in Microbiology. 2012;3:348.
24. Schmidt MW, Torn MS, Abiven S. Persistence of soil organic matter as an ecosystem property. Nature. 2011;478(7367):49-56.
25. Simpson AJ, Simpson MJ, Smith E. Microbially derived inputs to soil organic matter: are current estimates too low? Environmental Science & Technology. 2007;41(23):8070-6.
26. Six J, Bossuyt H, Degryze S. A history of research on the link between (micro)aggregates, soil biota, and soil organic matter dynamics. Soil and Tillage Research. 2006;79(1):7-31.
27. Smith AP, Marín-Spiotta E, Balser T. Microbial carbon use efficiency and soil organic matter stability across agricultural land uses. Biogeochemistry. 2018;140(1):91-105.
28. Wilson GW, Rice CW, Rillig MC. Long-term grassland restoration enhances microbial carbon contributions. Applied Soil Ecology. 2021;168:104115.
29. Zhang X, Amelung W, Yuan Y. Land-use effects on amino sugars in particle size fractions of an Argiudoll. Applied Soil Ecology. 2018;11(2):27-42.
30. Zhou J, Xue K, Xie J. Microbial mediation of carbon-cycle feedbacks to climate warming. Nature Climate Change. 2012;2(2):106-10.
31. Anderson TH, Domsch KH. Ratios of microbial biomass carbon to total organic carbon in arable soils. Soil Biology and Biochemistry. 2016;48(4):426-35.
32. Baldrian P, Kolařík M, Štursová M. Active and total microbial communities in forest soil are largely different and highly stratified during decomposition. ISME Journal. 2013;6(2):248-58.
33. Fierer N, Strickland MS, Liptzin D. Global patterns in belowground communities. Ecology Letters. 2009;12(11):1238-49.
34. Frey SD, Lee J, Melillo JM. The temperature response of soil microbial efficiency and its feedback to climate. Nature Climate Change. 2013;3(4):395-8.
35. Grandy AS, Neff JC. Molecular C dynamics downstream: the biochemical decomposition sequence and its impact on soil organic matter structure and function. Science of the Total Environment. 2008;404(2-3):297-307.
36. Kaiser K, Kalbitz K. Cycling downwards – dissolved organic matter in soils. Soil Biology and Biochemistry. 2012;52:29-32.
37. Lehmann J, Kleber M. The contentious nature of soil organic matter. Nature. 2015;528(7580):60-68.
38. Miltner A, Bombach P, Schmidt-Brücken B. SOM genesis: microbial biomass as a significant source. Biogeochemistry. 2012;111(1-3):41-55.

39. Sokol NW, Sanderman J, Bradford MA. Pathways of mineral-associated soil organic matter formation: integrating the role of plant carbon source, chemistry, and point of entry. Global Change Biology. 2019;25(1):12-24.
40. Throckmorton HM, Bird JA, Monte N. The source of microbial C has little impact on soil organic matter stabilisation in forest ecosystems. Ecology Letters. 2015;18(1):1-10.