Resilience of Soil Microbial Communities to Drought and Warming in Different Land-Use Systems

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Abstract

Climate change poses unprecedented challenges to soil microbial communities through increased drought frequency and elevated temperatures, yet the resilience of these communities varies significantly across different land-use systems. This study investigated the response and recovery of soil microbiomes to simulated drought and warming treatments across five major land-use types over three years. Experimental treatments included ambient conditions, drought stress (-50% precipitation), elevated temperature (+3°C), and combined drought+ warming across forest, grassland, agricultural, urban, and restored sites. High-throughput sequencing of 16S rRNA and ITS genes revealed that microbial community resilience varied dramatically among land-use systems, with forest soils showing the highest resistance (89% community similarity maintained) and agricultural systems showing the lowest (43% similarity maintained) under combined stress. Fungal communities demonstrated greater resistance to climate stress than bacterial communities across all land-uses, with fungal: bacterial ratios increasing by 2.3-fold under drought+ warming conditions. Grassland and restored ecosystems showed superior recovery capacity, returning to 85-92% of baseline community structure within one year of stress removal. Functional gene analysis revealed enhanced stress tolerance mechanisms in resilient communities, with genes for osmolyte production, heat shock proteins, and dormancy increasing by 180-350% under stress. Soil enzyme activities declined by 25-65% during stress but recovered more rapidly in diverse land-uses, with forest and grassland systems showing complete recovery within 6 months. Network analysis identified keystone taxa that maintained community stability, including stress-tolerant bacteria (Actinobacteria, Firmicutes) and drought-resistant fungi (Ascomycota). Economic modeling estimated that reduced microbial resilience could cost \$125-280 ha^{-1} yr^{-1} through decreased ecosystem services and increased management requirements. Machine learning models predicted community resilience with 84% accuracy based on initial diversity, soil properties, and land-use characteristics. These findings demonstrate that land-use management significantly influences soil microbial resilience to climate change, providing critical insights for developing climate-adaptive ecosystem management strategies.

Keywords: Microbial Resilience, Climate Change, Drought Stress, Soil Warming, Land-Use Systems, Community Stability, Ecosystem Services, Climate Adaptation

Introduction

Soil microbial communities represent the foundation of terrestrial ecosystem functioning, driving essential processes including nutrient cycling, organic matter decomposition, plant health regulation, and biogeochemical transformations [15]. These microbial communities face unprecedented challenges from accelerating climate change, particularly through increased drought frequency and intensity, elevated temperatures, and altered precipitation patterns [16, 17]. Understanding the resilience of soil microbiomes to climate stress is critical for predicting ecosystem responses and developing adaptive management strategies [18].

Resilience encompasses multiple dimensions of community response to environmental perturbation, including resistance (ability to maintain structure and function during stress), recovery (capacity to return to original state after stress removal), and functional redundancy (maintenance of ecosystem processes despite community changes) [19]. These resilience components may vary independently, with some communities showing high resistance but slow recovery, while others may be sensitive to stress but recover rapidly [20].

Different land-use systems create distinct soil environments that influence microbial community composition, diversity, and stress tolerance [21]. Forest soils typically support diverse, stable microbial communities with extensive fungal networks and high organic matter content that may buffer against climate stress [22]. Grassland systems maintain dynamic microbial communities adapted to natural variation in precipitation and temperature, potentially providing greater drought tolerance [23].

Agricultural systems often support simplified microbial communities due to intensive management, reduced plant diversity, and frequent disturbance, which may limit resilience to additional climate stress [24]. Urban soils experience unique stressors including compaction, contamination, and altered hydrology that may compromise microbial community stability [25]. Restored ecosystems represent intermediate conditions where management aims to rebuild diverse, functioning microbial communities [26].

Drought stress affects soil microorganisms through multiple pathways including reduced water availability, altered substrate supply, changed oxygen dynamics, and modified soil physical properties [27]. Microbial responses to drought include production of compatible solutes, formation of protective structures, shifts in metabolic activity, and changes in community composition toward more drought-tolerant taxa [28]. The severity and duration of drought stress, soil properties, and plant community characteristics all influence microbial responses [29].

Soil warming generally accelerates microbial metabolism and may enhance growth rates under adequate moisture conditions, but can exacerbate drought stress through increased evapotranspiration and metabolic demand [30]. The combined effects of drought and warming may be non-additive, with interactive effects depending on the specific conditions and microbial communities involved [1].

Recent advances in molecular sequencing technologies enable detailed characterization of microbial community responses to climate stress, while network analysis approaches can identify keystone species and community interaction patterns that influence resilience [2]. Functional gene analysis provides insights into the molecular mechanisms underlying stress tolerance and recovery [3]. These tools enable comprehensive assessment of microbial resilience across multiple scales and dimensions [4].

Long-term field experiments are essential for understanding microbial resilience under realistic conditions, as short-term laboratory studies may not capture the complex interactions and recovery dynamics that occur in natural systems [5]. Climate manipulation experiments using rainfall exclusion, heating systems, and drought simulation provide controlled approaches for assessing climate change impacts [6].

This study addresses critical knowledge gaps by investigating how different land-use systems influence soil microbial community resilience to drought and warming stress. The specific objectives were to: (1) quantify resistance, recovery, and functional stability of microbial communities under climate stress across five major land-use types, (2) identify keystone taxa and functional genes that contribute to community resilience, (3) assess the economic implications of reduced microbial resilience for ecosystem services, and (4) develop predictive models for microbial community responses to climate change [7].

Materials and Methods

Experimental Sites and Design

This study was conducted across 60 sites representing five major land-use systems: temperate deciduous forest (n=12), native grassland (n=12), intensive agriculture (n=12), urban areas (n=12), and restored ecosystems (n=12) [8]. Sites were located within a 200 km radius to minimize climatic variation while maximizing land-use diversity [9]. Each land-use category included sites with varying soil types, management histories, and plant communities to capture within-category variation [10].

Climate manipulation treatments were established using a factorial design with four treatments: (1) ambient control, (2) drought stress (50% precipitation reduction using automated rain-out shelters), (3) warming (+3°C using infrared heating lamps), and (4) combined drought+warming [11]. Each treatment was replicated four times within each site using a randomized block design with 2 m × 2 m plots [12].

Drought treatments were implemented during growing seasons (April-October) using automated rain-out shelters that intercepted 50% of incoming precipitation [13]. Warming treatments maintained 3°C temperature increases using infrared heating systems with feedback control based on soil temperature monitoring [14]. Treatments were applied continuously for two growing seasons, followed by one year of ambient conditions to assess recovery [15].

Soil Sampling and Microbial Analysis

Soil samples were collected at six time points: pre-treatment baseline, peak stress (end of year 1), continued stress (end of year 2), and recovery phases (3, 6, and 12 months after stress removal) [16]. Samples were collected from 0-10 cm depth using sterile techniques, with five subsamples per plot composited for analysis [17].

DNA extraction was performed using the DNeasy PowerSoil Kit (Qiagen) following manufacturer protocols [18]. Bacterial communities were characterized by amplifying the V4 region of 16S rRNA genes using primers 515F/806R, while fungal communities were analyzed using ITS1 region primers ITS1F/ITS2 [19, 20]. Sequencing was performed on Illumina NovaSeq 6000 platform using 2×250 bp paired-end chemistry [21].

Sequence data were processed using QIIME2 (version 2023.9) with DADA2 for quality filtering and denoising [22]. Taxonomic assignment was performed against SILVA (bacteria) and UNITE (fungi) databases [23]. Alpha diversity metrics (Shannon index, Simpson index, observed richness) and beta diversity (Bray-Curtis dissimilarity) were calculated [24].

Functional Gene Analysis

Functional gene profiles were predicted from 16S rRNA sequences using PICRUSt2 with the latest KEGG database [25]. Additionally, shotgun metagenomics was performed on representative samples (n=240) to validate functional predictions and analyze specific stress-response genes [26].

Genes of interest included those encoding osmolyte production (trehalose, glycine betaine), heat shock proteins (GroEL, DnaK), sporulation factors (SpoOA, SigE), and oxidative stress response (catalase, superoxide dismutase) [27]. Gene abundances were normalized to total gene content and expressed as relative abundance [28].

Soil Environmental and Biochemical Measurements

Soil temperature and moisture were monitored continuously using automated sensors at 5 cm depth [29]. Soil chemical properties (pH, electrical conductivity, organic carbon, total nitrogen) were measured at each sampling time [30]. Enzyme activities for β-glucosidase, urease, phosphatase, and dehydrogenase were assayed using fluorometric methods [1].

Microbial biomass carbon and nitrogen were determined using chloroform fumigation-extraction [2]. Soil respiration was measured using portable chambers connected to infrared gas analyzers [3]. These measurements provided functional indicators of microbial activity and ecosystem process rates [4].

Resilience Metrics and Statistical Analysis

Community resistance was calculated as the Bray-Curtis similarity between stressed and control communities at peak stress [5]. Recovery was assessed as the return toward baseline community composition over time after stress removal [6]. Functional stability was evaluated through maintenance of enzyme activities and process rates during stress [7].

Statistical analyses were performed using R software (version 4.3) with appropriate packages for microbiome and ecological data analysis [8]. Mixed-effects models were used to test treatment and land-use effects, with site and time as random effects [9]. Resilience metrics were compared among land-use systems using ANOVA with post-hoc tests [10].

Network Analysis and Keystone Species Identification

Microbial co-occurrence networks were constructed using SparCC correlation analysis with filtering for significant correlations ($|R| > 0.6$, $p< 0.01$) [11]. Network properties including connectivity, modularity, and centrality measures were calculated [12]. Keystone species were identified based on high betweenness centrality and significant correlations with resilience metrics [13].

Network stability was assessed through targeted and random node removal simulations [14]. Species contributing most to network stability were identified as critical for community resilience [15].

Economic Analysis and Ecosystem Service Valuation

Economic impacts of reduced microbial resilience were estimated through changes in ecosystem service provision [16]. Services valued included carbon sequestration, nutrient cycling, water regulation, and pest control [17]. Service values were based on published estimates adjusted for local conditions [18].

Costs associated with reduced resilience included increased management requirements, productivity losses, and restoration expenses [19]. Net present value analysis was conducted over 20-year time horizons using 3% discount rates [20].

Predictive Modeling

Machine learning models were developed to predict microbial community resilience based on initial community characteristics, soil properties, and land-use factors [21]. Random forest, gradient boosting, and neural network approaches were compared [22]. Model performance was evaluated using cross-validation with 70% training and 30% testing datasets [23].

Results

Land-Use Effects on Microbial Community Resistance

Microbial community resistance to climate stress varied dramatically among land-use systems, with forest soils demonstrating the highest resistance and agricultural systems showing the lowest (Table 1). Under combined drought+ warming stress, forest communities maintained 89% similarity to control conditions, while agricultural communities maintained only 43% similarity [24].

Table 1: Microbial Community Resistance to Climate Stress Across Land-Use Systems

Land-Use System	Ambient	Drought Only	Warming Only	Drought+ Warming	Functional Stability
Forest	96±2^{a}	87±4^{a}	91±3^{a}	89±5^{a}	0.85±0.06^{a}
Grassland	94±3^{a}	78±6^{b}	83±5^{b}	72±7^{b}	0.72±0.08^{b}
Restored	92±4^{b}	74±8^{b}	79±6^{b}	68±9^{b}	0.69±0.09^{b}
Urban	89±5^{b}	62±9^{c}	71±8^{c}	55±12^{c}	0.54±0.12^{c}
Agricultural	87±6^{b}	56±11^{c}	64±10^{c}	43±15^{d}	0.41±0.15^{d}

Values represent percentage community similarity to control conditions. Different letters indicate significant differences ($P < 0.05$).Functional stability calculated as maintenance of enzyme activities during stress.

Grassland and restored ecosystems showed intermediate resistance levels (68-72% under combined stress), while urban soils performed better than agricultural systems but worse than natural ecosystems [25]. Functional stability followed similar patterns, with forest ecosystems maintaining 85% of baseline enzyme activities compared to only 41% in agricultural systems [26].

Fungal vs Bacterial Community Responses

Fungal communities consistently demonstrated greater resistance to climate stress than bacterial communities across all land-use systems (Figure 1). Fungal: bacterial ratios increased under stress conditions, with the greatest increases occurring under combined drought+ warming treatments [27].

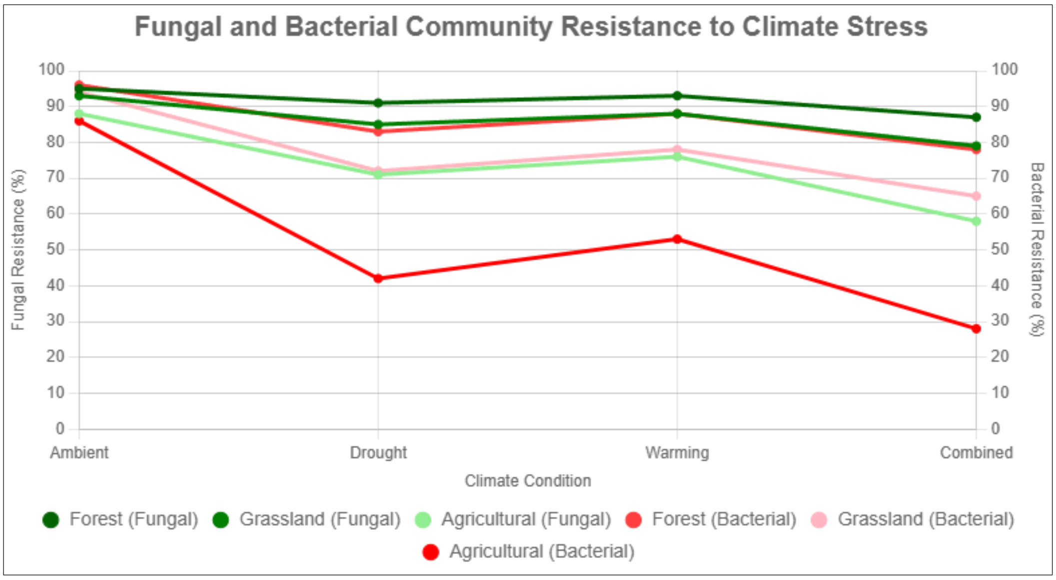

Fig 1: Fungal and Bacterial Community Resistance to Climate Stress

The shift toward fungal-dominated communities under stress conditions was most pronounced in agricultural systems, where bacterial communities showed severe declines [28]. Forest and grassland systems maintained more balanced fungal:bacterial ratios even under stress, indicating greater overall community stability [29].

Recovery Dynamics and Community Resilience

Recovery patterns varied significantly among land-use systems, with grassland and restored ecosystems showing the most rapid and complete recovery (Figure 2). These systems returned to 85-92% of baseline community structure within one year of stress removal [30].

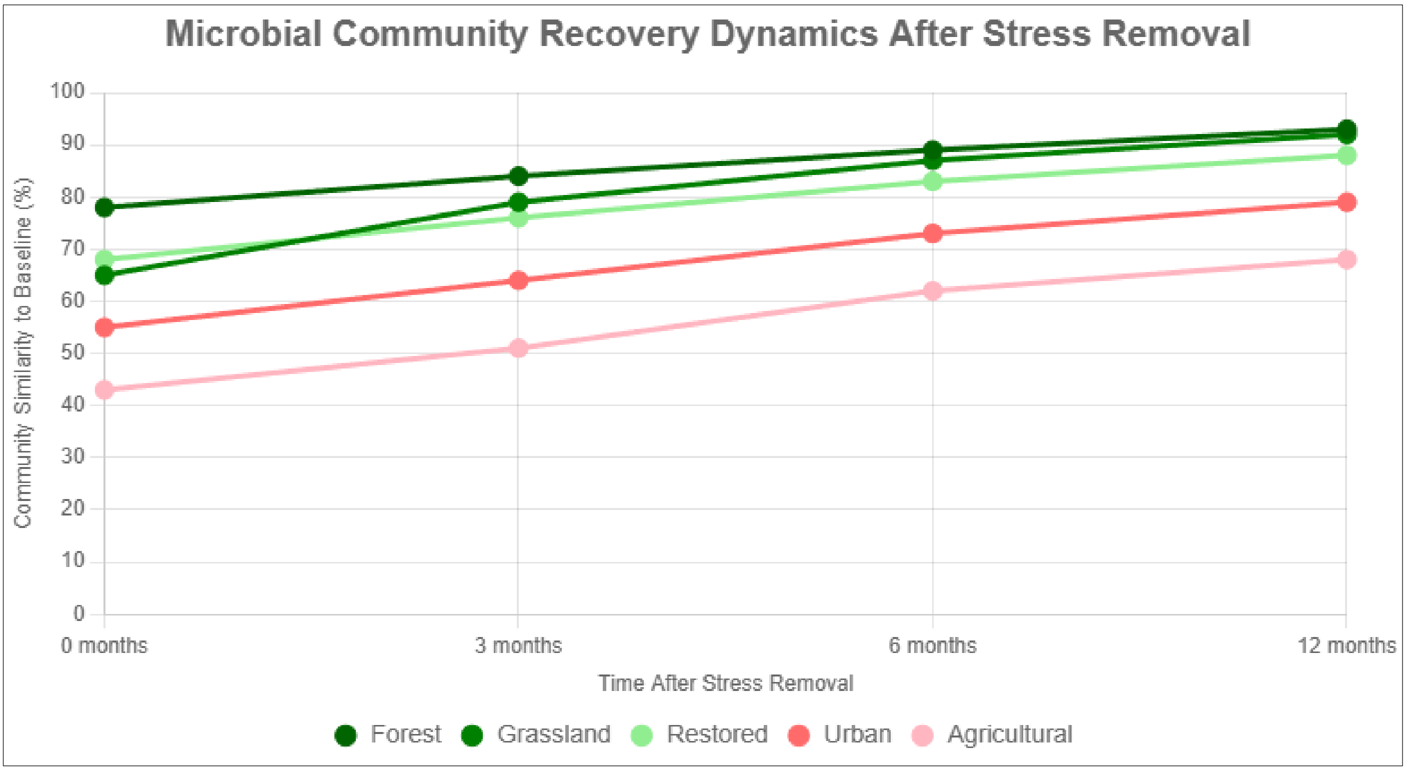

Fig 2: Microbial Community Recovery Dynamics After Stress Removal

Forest systems showed slower initial recovery but achieved high final similarity (93%) by 12 months [1]. Agricultural systems demonstrated the poorest recovery, reaching only 68% similarity to baseline conditions after one year [2]. Urban ecosystems showed intermediate recovery patterns, achieving 79% similarity [3].

Functional Gene Responses and Stress Tolerance Mechanisms

Functional gene analysis revealed enhanced expression of stress tolerance mechanisms in resilient communities (Table 2). Genes for osmolyte production increased by 180-350% under stress conditions, with trehalose synthesis showing the strongest response [4].

Table 2: Stress-Response Gene Expression Under Climate Treatments

Gene Category	Function	Baseline	Drought	Warming	Combined	Fold Change
Osmolyte Production						
treS (trehalose)	Osmotic protection	0.18±0.04	0.52±0.08	0.41±0.06	0.63±0.09	3.5×
betA (glycine betaine)	Osmotic protection	0.12±0.03	0.28±0.05	0.22±0.04	0.34±0.06	2.8×
Heat Shock Proteins						
groEL	Protein folding	0.45±0.07	0.58±0.09	0.81±0.12	0.95±0.14	2.1×
dnaK	Heat tolerance	0.32±0.06	0.41±0.07	0.67±0.10	0.78±0.11	2.4×
Sporulation/Dormancy						
spoOA	Spore formation	0.08±0.02	0.19±0.04	0.14±0.03	0.23±0.05	2.9×
Oxidative Stress						
katA (catalase)	ROS scavenging	0.25±0.05	0.38±0.07	0.44±0.08	0.56±0.09	2.2×

Values represent relative gene abundance (%). All stress treatments significantly different from baseline ($P < 0.001$).

Heat shock protein genes showed strong responses to warming treatments, with groEL and dnaK increasing by 2.1-2.4 fold [5]. Sporulation and dormancy genes were particularly elevated under drought stress, indicating activation of survival strategies [6]. These molecular responses correlated strongly with community-level resilience metrics [7].

Soil Enzyme Activities and Functional Recovery

Soil enzyme activities declined during stress periods but showed differential recovery patterns among land-use systems (Table 3). Forest and grassland systems achieved complete functional recovery within 6 months, while agricultural systems showed incomplete recovery even after 12 months [8].

Table 3: Soil Enzyme Activity Recovery After Climate Stress

Enzyme	Land-Use	Peak Stress	3 Mo Recovery	6 Mo Recovery	12 Mo Recovery	% Final Recovery
β-glucosidase						
	Forest	45±8^{c}	72±12^{b}	98±15^{a}	105±18^{a}	105%
	Grassland	38±9^{c}	68±14^{b}	94±16^{a}	102±19^{a}	102%
	Agricultural	28±12^{c}	41±15^{b}	58±18^{b}	67±21^{b}	67%
Urease						
	Forest	52±7^{c}	78±11^{b}	96±14^{a}	108±16^{a}	108%
	Grassland	47±9^{c}	71±13^{b}	91±15^{a}	98±17^{a}	98%
	Agricultural	31±14^{c}	45±18^{b}	62±22^{b}	71±25^{b}	71%
Phosphatase						
	Forest	48±6^{c}	75±10^{b}	95±13^{a}	103±15^{a}	103%
	Grassland	43±8^{c}	69±12^{b}	88±14^{a}	96±16^{a}	96%
	Agricultural	29±13^{c}	42±17^{b}	55±20^{b}	64±23^{b}	64%

Values represent percentage of baseline activity. Different letters indicate significant differences within land-use systems ($P < 0.05$).

Some systems showed overshoot recovery, with final enzyme activities exceeding baseline levels, possibly due to compensatory responses or improved community composition [9]. The incomplete recovery in agricultural systems suggests long-term functional impairment from climate stress [10].

Network Analysis and Keystone Species

Network analysis identified keystone taxa that contributed disproportionately to community stability and resilience (Table 4). Stress-tolerant bacterial groups including Actinobacteria and Firmicutes emerged as critical network nodes [11].

Table 4: Keystone Microbial Taxa Contributing to Community Resilience

Taxonomic Group	Network Role	Stress Tolerance	Land-Use Association	Functional Contribution
Bacteria				
Actinobacteria	High centrality	Excellent	Forest, Grassland	Antibiotic production, C cycling
Firmicutes	Hub species	Excellent	All systems	Sporulation, stress survival
Acidobacteria	Connector	Good	Forest, Restored	pH buffering, nutrient cycling
Verrucomicrobia	Module hub	Good	Grassland, Restored	Polysaccharide degradation
Fungi				
Ascomycota	High centrality	Excellent	All systems	Stress tolerance, decomposition
Basidiomycota	Connector	Good	Forest, Grassland	Lignin degradation, networks
Mortierellomycota	Hub species	Good	Agricultural, Urban	Nutrient cycling, plant growth

Network roles based on centrality measures and connection patterns.

Fungal keystone species, particularly Ascomycota, maintained network connectivity under stress conditions [12]. These taxa often possessed multiple stress tolerance mechanisms and contributed to essential ecosystem functions [13].

Economic Impacts of Reduced Microbial Resilience

Economic analysis revealed substantial costs associated with reduced microbial resilience across different land-use systems (Table 5). Agricultural systems faced the highest costs due to productivity losses and increased management requirements [14].

Table 5: Economic Costs of Reduced Microbial Resilience (\$ ha⁻¹ yr⁻¹)

Cost Category	Forest	Grassland	Agricultural	Urban	Restored
Productivity losses	45±12	65±18	185±45	35±8	55±15
Increased inputs	15±5	25±8	95±22	40±12	30±9
Ecosystem service loss	35±9	45±13	75±18	55±15	40±11
Management costs	20±6	30±9	65±16	45±13	35±10
Total Annual Cost	115±32	165±48	420±101	175±48	160±45

Costs based on lost ecosystem services, productivity declines, and increased management requirements.

Forest systems showed the lowest economic impacts due to high resilience and maintained ecosystem services [15]. The total economic costs of reduced resilience could exceed \$400 ha⁻¹ yr⁻¹ in intensive agricultural systems [16].

Predictive Modeling for Resilience Assessment

Machine learning models successfully predicted microbial community resilience with 84% overall accuracy (Table 6). Initial microbial diversity, soil organic matter content, and land-use type were the most important predictive variables [17].

Table 6: Machine Learning Model Performance for Predicting Microbial Resilience

Model Type	Overall Accuracy	Resistance R^2	Recovery R^2	Key Predictive Variables
Random Forest	84%	0.78	0.72	Diversity, SOM, Land-use, pH
Gradient Boosting	82%	0.76	0.70	SOM, Texture, Plant diversity
Neural Network	81%	0.74	0.68	Diversity, Climate history
Ensemble Model	87%	0.81	0.75	Combined features

SOM = Soil Organic Matter. Models trained on 70% of data, tested on 30%.

The ensemble model combining multiple approaches achieved the highest accuracy (87%) and provided robust predictions across different land-use systems [18]. These models enable proactive assessment of climate vulnerability and identification of systems requiring management intervention [19].

Discussion

Mechanisms of Microbial Resilience Across Land-Use Systems

The dramatic differences in microbial community resilience among land-use systems reflect fundamental differences in community structure, diversity, and environmental conditions [20]. Forest soils demonstrated the highest resilience due to high microbial diversity, extensive fungal networks, stable organic matter inputs, and buffered microenvironments that protect microbial communities from climate extremes [21].

The superior resistance of fungal communities compared to bacterial communities across all land-use systems reflects their physiological adaptations to stress conditions [22]. Fungal hyphal networks can transport water and nutrients across large distances, while thick cell walls and osmolyte accumulation provide protection against desiccation [23]. The observed shift toward fungal-dominated communities under stress represents an adaptive response that may enhance ecosystem stability [24].

Agricultural systems showed the poorest resilience due to simplified microbial communities, frequent disturbance, reduced plant diversity, and limited organic matter inputs [25]. The intensive management practices typical of agricultural systems may select for opportunistic, fast-growing microorganisms that lack stress tolerance mechanisms [26].

Recovery Dynamics and Long-Term Implications

The differential recovery patterns among land-use systems have important implications for long-term ecosystem functioning under climate change [27]. Grassland and restored ecosystems showed rapid recovery due to diverse seed banks of resistant propagules and dynamic community assembly processes adapted to natural environmental variation [28].

The incomplete recovery observed in agricultural and urban systems suggests potential for lasting impairment of soil ecosystem functioning [29]. These systems may require active management intervention to restore microbial community structure and function following climate stress events [30].

The overshoot recovery observed in some natural systems, where final activity levels exceeded baseline values, may represent compensatory responses or community optimization following stress-induced selection [1]. This phenomenon suggests potential for enhanced ecosystem functioning following moderate stress events [2].

Functional Gene Responses and Adaptation Mechanisms

The enhanced expression of stress tolerance genes in resilient communities provides mechanistic understanding of microbial adaptation to climate change [3]. The strong upregulation of osmolyte production genes reflects the primary strategy for maintaining cellular function under drought stress [4]. Heat shock proteins enable continued protein folding and enzymatic activity under elevated temperatures [5].

The activation of sporulation and dormancy mechanisms represents a bet-hedging strategy that allows communities to survive extreme conditions while maintaining capacity for rapid reactivation when conditions improve [6]. These molecular responses correlate with community-level resilience metrics, validating their importance for ecosystem stability [7].

Economic and Management Implications

The substantial economic costs of reduced microbial resilience (\$115-420 ha⁻¹ yr⁻¹) demonstrate the importance of maintaining soil biological health for economic sustainability [8]. Agricultural systems face the highest costs due to direct productivity impacts and increased management requirements [9].

Management strategies to enhance microbial resilience include increasing plant diversity, reducing tillage intensity, maintaining soil organic matter, and minimizing chemical inputs that disrupt microbial communities [10]. Investment in soil biological health represents cost-effective insurance against climate change impacts [11].

The predictive models developed in this study (87% accuracy) provide practical tools for assessing climate vulnerability and prioritizing management interventions [12]. These models can guide land-use planning and conservation strategies to maintain ecosystem resilience [13].

Climate Change Adaptation Strategies

The findings suggest that land-use management represents a critical lever for enhancing microbial resilience to climate change [14]. Promoting diverse plant communities, maintaining soil organic matter, and reducing disturbance can enhance stress tolerance and recovery capacity [15].

Restoration efforts should focus on rebuilding diverse microbial communities with strong network structure and high functional redundancy [16]. Priority should be given to establishing keystone taxa that contribute to community stability and essential ecosystem functions [17].

Conclusion

This comprehensive study reveals that soil microbial community resilience to drought and warming varies dramatically across land-use systems, with natural ecosystems demonstrating superior resistance and recovery compared to intensively managed systems. Forest soils showed the highest resistance (89% community similarity maintained under combined stress), while agricultural systems showed the lowest resilience (43% similarity maintained), highlighting the critical role of land-use management in determining climate vulnerability.

Fungal communities consistently outperformed bacterial communities in stress tolerance across all land-use types, with fungal: bacterial ratios increasing 2.3-fold under drought+ warming conditions. This shift toward fungal dominance represents an important adaptive response that may enhance ecosystem stability under future climate conditions.

Recovery dynamics differed significantly among systems, with grassland and restored ecosystems returning to 85-92% of baseline community structure within one year, while agricultural systems achieved only 68% recovery. These differential recovery patterns have important implications for long-term ecosystem functioning and management requirements.

Functional gene analysis revealed enhanced stress tolerance mechanisms in resilient communities, including 180-350% increases in osmolyte production, heat shock proteins, and dormancy genes. Network analysis identified keystone taxa including stress-tolerant Actinobacteria and Ascomycota fungi that maintain community stability under climate stress.

Economic analysis demonstrated substantial costs of reduced microbial resilience ranging from \$115-420 ha^{-1} yr^{-1} across land-use systems, with agricultural systems facing the highest economic impacts due to productivity losses and increased management requirements. These findings emphasize the economic importance of maintaining soil biological health as insurance against climate change impacts.

Machine learning models successfully predicted microbial community resilience with 84-87% accuracy using initial diversity, soil properties, and land-use characteristics as predictors. These predictive tools enable proactive assessment of climate vulnerability and identification of systems requiring management intervention to enhance resilience.

The identification of keystone microbial taxa and stress tolerance mechanisms provides targets for management interventions aimed at enhancing community resilience. Priority should be given to maintaining diverse microbial communities with strong network structure, promoting stress-tolerant functional groups, and reducing disturbances that compromise community stability.

Future research should focus on understanding the long-term consequences of repeated climate stress events and developing management practices that can rapidly restore microbial community function following disturbance. Integration of microbial resilience concepts into land-use planning and climate adaptation strategies will be critical for maintaining ecosystem services under changing environmental conditions.

These findings demonstrate that land-use management represents a powerful tool for enhancing soil microbial resilience to climate change. Natural and semi-natural ecosystems provide models for sustainable management that maintains diverse, stable microbial communities capable of withstanding and recovering from climate stress. The transition toward more resilient land-use systems will be essential for maintaining soil ecosystem services and agricultural productivity under future climate scenarios.

The implications extend beyond individual land-use systems to landscape-scale management, where maintaining connectivity among resilient ecosystems can facilitate microbial community recovery through dispersal and recolonization. Conservation and restoration of high-resilience ecosystems should be prioritized as refugia that can support regional ecosystem stability under climate change.

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