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Impact of climate change on microorganisms

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Abstract

The Earth contains approximately 1030 living cells, with a vast amount of these cells being microorganisms. These small organisms play a crucial role in understanding the inputs and impacts of climate change, as they play diverse roles in sequestering and producing greenhouse gases. In marine realms, microbes define global nutrient cycles and fix about half of the Earth's carbon. On land, microbes in soil regulate soil carbon storage directly while influencing plant life growth and productivity. The diverse roles of microbes in both sequestering and producing greenhouse gases raise concerns about the impacts of changing climate on the microbe-mediated carbon source-sink balance. Microbe-associated processes can be linked to high uncertainty and high risk, such as the release of large amounts of carbon dioxide and methane, which could trigger warming-carbon feedback loops.

Keywords: Global warming, climate alter, ocean acidification, adaptation, soil fertility

Introduction

Climate alter essentially impacts soil microbial communities, which are vital for environmental forms like primary productivity and nutrient cycling. Changes in plant communities, which too happen in response to temperature changes, can indirectly intervene the impacts of climate warming on biological capacities by influencing soil microbial biomass, community composition, and microbial turnover. Climate alter is unarguably a critical existential risk to humankind within the 21st century. Organisms are major drivers of natural cycles (such are carbon, nitrogen, and phosphorus), imperative producers and consumers of greenhouse gasses, and relevant pathogens of humans, animals, and plants. Whereas the risk of climate alter looms large, discussions almost the relationship between it and microorganisms are still uncommon exterior of the microbial sciences community. To understand completely how our climate may change within the future, it is vital to memorize how a changing climate will affect organisms and their connections with people and their environment, as well as join microbial forms into climate models.

Temperature effects

Soil thermals can directly or indirectly affect the microbial community by impacting soil moisture, nutrient availability, and vegetation growth. However, responding to soil thermals is intricate, and no definite conclusion on its impact and mechanism exists. As global climate warms gradually, an essential understanding is required to predict the response of microbial geochemical processes to soil thermals. An analysis found that the α diversity index of soil microorganisms decreased significantly with temperature increases, while the β diversity altered with temperature and ecosystem shifts. Most bacteria only change with higher rises in temperature.

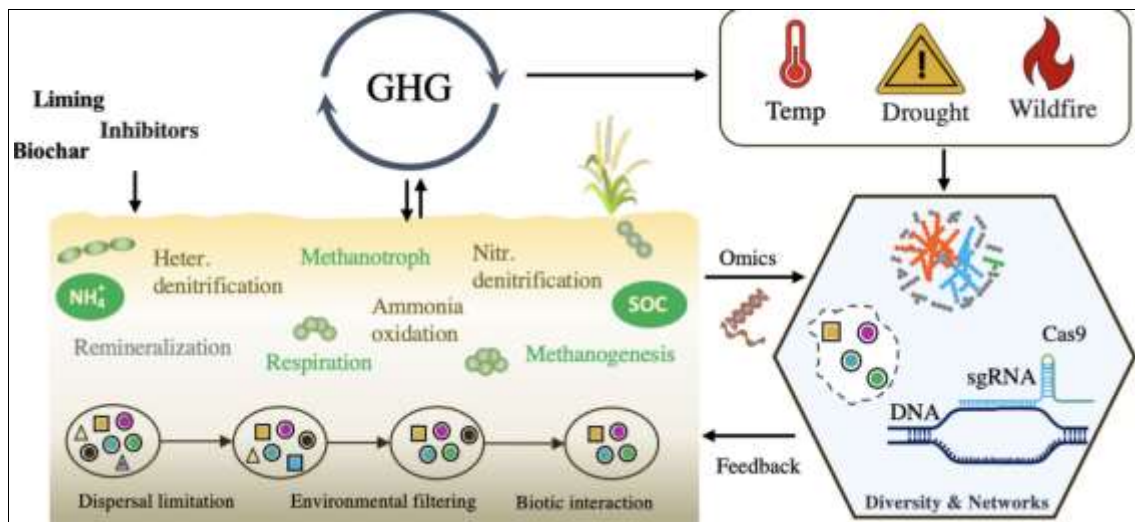
Soil thermals in wetland ecosystems are more sensitive to temperature increases, and bacteria changes were consistent with overall alterations. This analysis revealed significant changes in microbial community composition on soil thermals, with dominant microbiomes regulating nutrient and energy flow. A global perspective of temperature response is crucial for understanding how soil microbes change due to climate warming.

The projected global temperature increase, particularly in northern permafrost regions and the Tibetan Plateau, has substantial consequences for soil ecosystems, particularly microbial communities. Soil microorganisms are vital for soil ecosystem fertility and productivity, contributing to soil structure and stability through mucous substances production. They regulate C and N cycles, control litter decomposition, C mineralization, nutrient release, N nitrification and denitrification, and establish symbiotic associations with plants.

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Fig 1: Soil microbiome in response to heat and greenhouse gases resulting change in the genomic transcription

Temperature governs the growth and activity of soil microorganisms, propelling significant biochemical cycles. Microbial communities are sensitive to thermals, with only a few thermally adapted microbes dominating the community post-disturbances. Climate warmth affects soil microbial community composition, diversity, and interaction network complexity and stability. The effects of increasing soil temperature on soil microorganisms depend on abiotic conditions associated with nutrient cycling.

Extreme weather events

Drought

Drought is a significant climate phenomenon negatively impacting agricultural productivity and food security. Drought severity and frequency are expected to increase in the next decade, significantly affecting the soil microbiome, influenced by moisture and temperature. Reductions in labile carbon and nitrogen due to drought may result in the loss of microbial phyla such as Verrucomicrobia, Proteobacteria, and Acidobacteria, sensitive to nitrogen ratios.

Warming induced by drought can reduce the abundance of 16S rRNA genes in soil microorganisms seasonally. Plant roots' microbiomes change during drought, favoring Actinobacteria and other Gram-positive species, substituting predominantly present Gram-negative taxa. Actinobacteria and Firmicutes thrive in drought, while Acidobacteria thrive in acidic soils.

Soil microorganisms cope with drought stress using various techniques to maintain survival. They release compatible osmolytes as protective mechanisms, collect organic compounds reducing solute potential without interrupting cellular metabolism, and increase extracellular polymeric substance (EPS) synthesis as an effective drought adaptation method. Fungi are abundant and less impacted by drought due to their widespread hyphal development.

Antibiotics are produced at higher rates during drought stress as a physical reaction to compete for scarce resources with other bacteria or as triggers for drought response mechanisms such as biofilm formation. The increased availability of antibiotics during a drought could be due to rapid environmental changes leading to bacteria formation with drought-resistant traits.

Flood

Flooding in soil can altogether diminish O₂ concentration, change soil microbial community dispersion, and increment ethylene accumulation in plants. Soil organisms, such as Alphaproteobacteria, Betaproteobacteria, and Deltaproteobacteria, can survive submergence and appear quantifiable changes 7 days after flooding. Studies have appeared that anaerobic microscopic organisms, such as Anaeromyxobacter and Malikia, may only be display after flooding occasions, whereas obligate oxygen consuming microscopic organisms, like Xanthomonadaceae, vanish totally.

Soil microbial communities appear quantifiable changes 7 days after flooding and take 21-24 days to reach a steady community. Studies have appeared that Gram-negative microscopic organisms diminish beneath flooding with new water, whereas Gram-positive microscopic organisms increase. Inoculation of seeds with Gram-positive plant development promoting rhizobacteria can offer assistance rice varieties IR42 withstand submergence stretch by decreasing the inhibitory impact of ethylene stress.

Microscopic organisms have advanced ways to manage with push, such as actuating aquaporins, directing potassium transporters, and utilizing mechano-sensitive channels to maintain a strategic distance from cell lysis amid sudden osmotic weight. These channels sense pressure inside the cell layer instead of weight over it, discharging osmotically dynamic particles and solutes to stabilize cells.

Metal Toxicity

Anthropogenic mediations and over the top agrochemical application adversely affect soil microbial communities and functional diversity, driving to disintegration of soil wellbeing. Heavy metals, such as cadmium, lead, chromium, and mercury, can disturb the life cycle of living organisms by causing cell layer damage, enzymatic and cellular forms, and DNA structural damage. Soil organisms utilize these metals in metabolism as electron donors or acceptors, but they can be utilized in impressive amounts without harming them. Soil microbes in low-contamination soils utilize more carbon for absorption and produce more CO₂ amid the dissimilation process, contributing to worldwide temperatures. In any case, heavy metal contamination in mangrove wetland confines CO₂

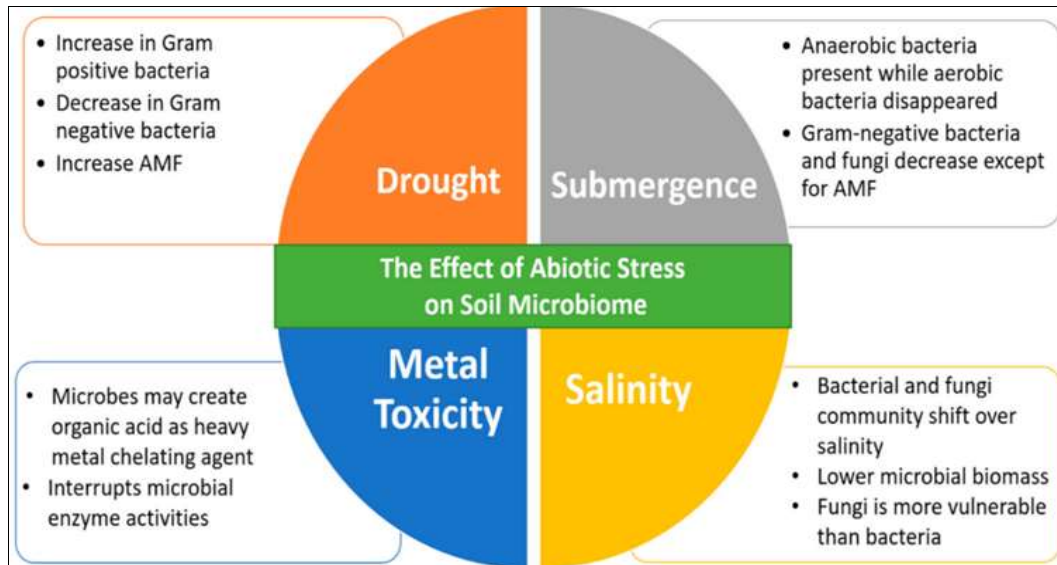
generation whereas advancing CH₄ fluxes. Firmicutes, Proteobacteria, and Actinobacteria predominately colonize heavy metal contaminated areas, whereas AMF as often as possible colonizes nutrient-poor soils contaminated with heavy metals. Organic acids, such as *Beauveria caledonica*, can solubilize heavy metals and stimulate microbial activity in the rhizosphere.

Cadmium hinders soil microorganisms' protein exercises, break down film structure, and meddling with protein amalgamation in cells. High pH, clay, and natural matter substance in soil lower Cd accessibility, making it more deadly on enzymes. Heavy metals can disturb microbial propagation and initiate morphological and physiological

abnormalities, posing a risk to human and natural wellbeing.

Salinity

Salinization could be a critical soil degradation issue, fundamentally caused by agricultural inputs like sewage slime, fertilizer, and civil plant waste items. This leads to high osmotic pressures, destructive particles, and nourishment imbalances, influencing plant advancement and soil organisms. Salinity influences soil processes, defining osmotic pressure and sodium content within the soil's exchange complex. Sodidity develops slowly from saltiness, with halophiles living in high saltiness situations and halotolerant organisms adjusting to saline situations.



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Fig 2: The effect of changes in environmental factors on the soil microbes

Halophilic microbes have salt-tolerance or salt-dependent catalytic properties, which can work in extraordinary conditions. These proteins are significant for plant-microbiome interaction and soil stability. Salt-tolerant plants have advantageous microbiomes in their rhizospheres, empowering them to develop and adapt against drought and extraordinary saltiness. Microorganisms and plants may accumulate osmolytes to adjust to low osmotic pressure, but this production costs vitality and includes a gigantic C-skeleton. Salinity brings down microbial action, relative abundance, and the shape of microbial communities due to their expansive range volume proportion, high penetrability of cell film, and fast turnover rate. Parasites are more defenseless to salt stretch, and saltiness resistance shifts among microorganisms, influencing the composition of microbial communities. The essential organic osmolytes are proline and glycine betaine, while the primary predominant inorganic substances utilized in salt-tolerant microscopic organisms are potassium ions. Synthesizing osmolytes from inorganic salts is hazardous, so only exclusive halophytic microorganisms with salt-tolerant enzymes can flourish in saline conditions (Abdul Rahman *et al.*, 2021) ^[1].

Territory Loss and Fragmentation

The study examines the affect of climate warming on the biogeochemical cycles of the environment within the Qinghai-Tibet Level. It found that reenacted warming significantly lowered ecosystem function within the

grassland but not within the shrubland. This inconsistency was due to the diverse responses of the different taxa display in each biological system to warming conditions and their contrasting parts in deciding and regulating ecosystem function. The microbial maintenance of ecosystem function was fundamentally dependent on the diversity of bacterial dominant taxa and conditionally rare taxa (CRT), and was less subordinate on always rare taxa (ART) and fungal taxa. Bacterial CRT and dominant taxa of the meadow environment were more sensitive to changing climatic conditions than grassland ART, coming about in a more articulated negative differing qualities response. Understanding the utilitarian characteristics and response characteristics of different taxa is pivotal for anticipating the impacts of climate alter on ecosystem function and informing environmental reconstruction efforts in elevated districts of the plateau. Climate alter essentially impacts soil microbial communities, which are vital for environmental forms like primary productivity and nutrient cycling. Changes in plant communities, which too happen in response to temperature changes, can indirectly intervene the impacts of climate warming on biological capacities by influencing soil microbial biomass, community composition, and microbial turnover. Microscopic organisms and fungi have diverse hereditary, physiological, and useful characteristics, driving to varying roles in soil environment working. Microbes exert a more prominent impact on soil functions in elevated meadows due to their

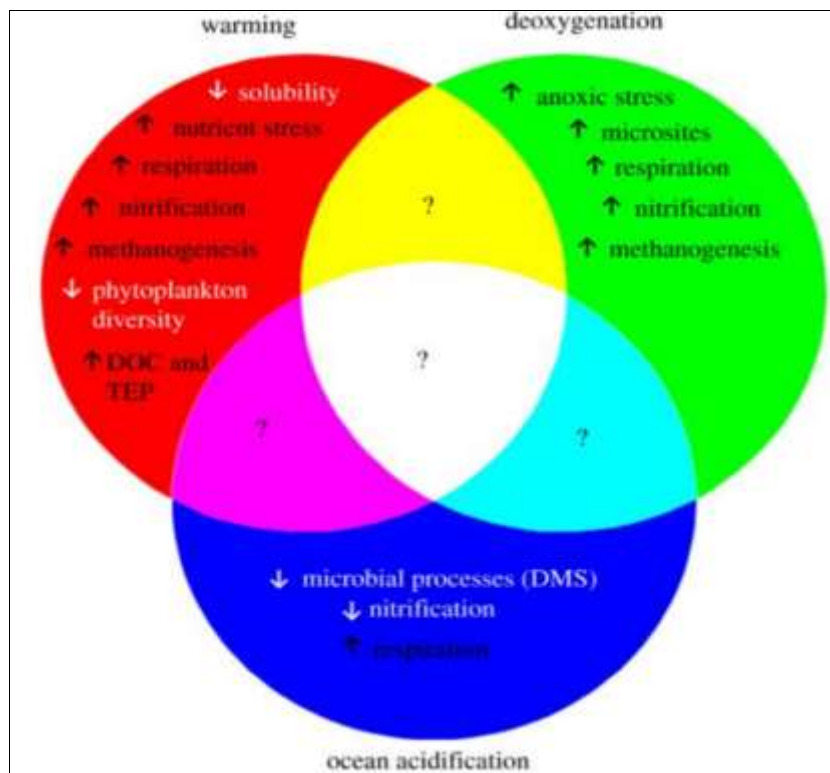
capacity to adjust to barren soils and favor decomposable substrates. In any case, advance examination is required to get it the relative significance of contagious and bacterial communities within the setting of rising temperatures on soil environment working. Soil microbial organisms have shown prove of phylogenetic preservation in their reactions to outside unsettling influences, but different responses among microbial taxa, counting uncommon and abundant taxa, can lead to changing impacts on soil biological system function. The basic driving force for biological system work comes from uncommon microbial taxa characterized by high diversity, which excessively contribute to fundamental organic processes.

Ocean Acidification

Ocean biogeochemical cycles and biological systems are dependent on three free components: rising temperatures, ocean acidification and ocean deoxygenation. Rising temperatures cause significant changes within the physical, chemical, and organic environment, influencing the ocean's biogeochemical cycles and environments in ways we are only beginning to understand. Ocean warming will specifically influence organisms and biogeochemical cycles, whereas expanding upper ocean stratification. Ocean acidification, caused by the uptake of anthropogenic carbon dioxide, will influence numerous organisms and forms, in spite of the fact that the precise degree of this effect is not accurately estimated yet. Ocean deoxygenation, the loss of dissolved oxygen, will happen in a warming and more stratified sea, causing stress to the local flora and fauna that depend on adequate oxygen levels. These stressors will work all inclusive, with distinct territorial contrasts. High latitudes will experience the strongest impacts of ocean acidification, whereas low-oxygen regions are most prone to

deoxygenation. Synergistic impacts, such as changes in organic matter traded to the ocean's insides, seem to cause considerable oxygen concentration changes. Sea warming, acidification, and deoxygenation are irreversible on centennial time scales, and the essential mitigation strategy is to diminish CO₂ emanation. Ocean acidification (OA) isn't a standalone issue but or maybe portion of a bigger worldwide natural alter. The ocean has taken up 28% of the overabundance anthropogenic CO₂ since 1750 and retained 93% of the overabundance warm over the past 45 years. This changes altogether modify the physical and chemical environment experienced by marine organisms, such as expanding organic rates and diminishing worldwide sea oxygen inventories.

Warming and refreshing moreover upgrade surface sea stratification, which diminishes blended layer depth and decreases supplement entrainment into the euphotic layer. This comes about in higher levels of irradiance experienced by life forms, alleviating light confinement at high latitudes but enhancing nutrient limitation at low- to mid-latitudes. CO₂-driven changes in seawater carbonate chemistry occur simultaneously with warming, deoxygenation, localized rousing of the sea, and changes to supplement dynamics. However, few demonstrating studies have centered on trace gas emanations and OA-related feedbacks to the soil framework. Two studies have utilized electronic supplementary material to supply prove for a potential positive climate criticism emerging from pH-sensitivity of DMS (dimethylsulfide) production. Both studies uncovered critical radiative constraining and surface warming in response to diminished DMS flux to the climate and ensuing changes in airborne and cloud properties (Hopkins FE *et al.*, 2019) [6].



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Fig 3: Disbalance shown in microbial activity and growth due to OA, global warming and deoxygenation. In conclusion, OA is a complex and interconnected global environmental change that impacts marine ecosystems and biogeochemistry

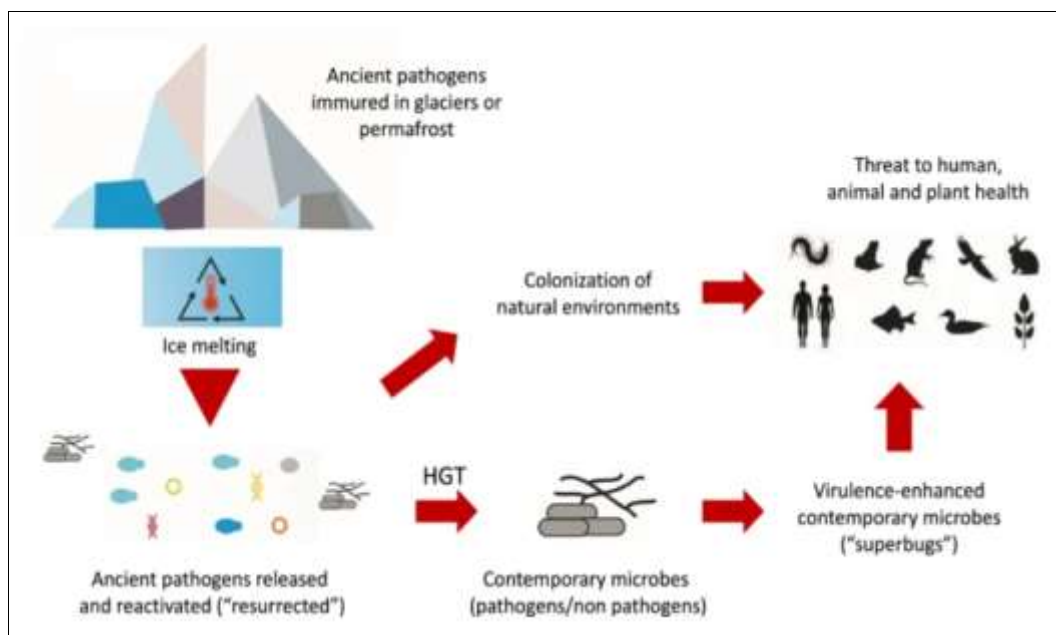
Glacial retreat

Solidified ones, are rich in qualities, especially antibiotic-resistant microorganisms. Ice sheets, indeed the foremost perfect and farther ones, have been found to contain an bewildering sum of antibiotic-resistant microorganisms that can thrive *in vitro* within the presence of high dosages of anti-microbials once reactivated. Antibiotic resistant genes (ARG) have been frequently recognized in old microbes isolated from for all time solidified environments. For illustration, microbes from eastern siberian permafrost sediments, collected at central Yakutia, were found to carry different ARG. (D'costa *et al.*, 2011) [17] moreover detected ARG in permafrost tests from the frozen north, matured 30,000 years-old, that encoded resistance to β -lactams, tetracycline, and glycopeptide anti-microbials.

A especially concerning event is the occurrence of microscopic organisms carrying integrons in tests collected from distant and farther ice sheets. These complex hereditary components can capture qualities and quality cassettes, frequently encoding for anti-microbial resistance. Integrons are at the origin of multidrug resistance in microbes. Sequence-based metagenomics has been the

preferred procedure to distinguish numerous ARGs or complex hereditary components and predict the resistant potential of microbial communities colonizing flawless ecosystems. Functional metagenomics has moreover made a difference to secure the diversity of environmental genes, hereditary components, and mechanisms behind resistance to anti-microbials in ecosystems not subjected to anthropogenic disturbances.

Ancient antimicrobial resistance genes (ARGs) have been found to hold their work in both homologous and heterologous hosts. However, the link between environmental ARG and antibiotic-resistant human pathogens is unclear. More endeavors should be made to test the hypothesis that a few ancient ARGs might be transmitted to modern microbes by horizontal gene transfer (HGT). A point of interest within the study of old ARGs was the separation and sequencing of plasmids extracted from old permafrost microbes, aged 15,000 to 40,000 years-old. One of these plasmids contained streptomycin and tetracycline resistance determinants, which were transferred to "advanced" plasmids, confirming their capacity to spread into modern characteristic bacterial populations.



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Fig 4: Ancient pathogens released and reactivated due to excessive heat and climate change.

It is accepted that following ice defrosting, a few of these ARG-containing hereditary components could be exchanged evenly to present day organisms, giving rise to new strains of multi- and pan-resistant "superbugs." Infections colonizing forever solidified habitats exhibit surprising ordered- and utilitarian diversities and play vital parts in controlling the population elements of prokaryotic communities and biogeochemical cycles inside solidified situations. The sum of virus-like-particles (VLP) totally different cold situations has been extend between $0.9 \times 10^6 \text{ ml}^{-1}$ and $3.1 \times 10^7 \text{ ml}^{-1}$ (Yarzabal *et al.*, 2021) [13].

Modified biogeochemical cycles

The study examines the impact of heat and freeze-thaw disturbances on microbial processes and community composition. It hypothesizes that transitory disturbances

lead to a more rapid cycling of carbon, nitrogen, and phosphorus (c), nitrogen, and phosphorus (n) due to immediate mineralization bursts following drying-rewetting or freeze-thaw events. In any case, the study found expanded microbial respiration after transitory temperature disturbances, but microbial nitrogen forms were generally steady, especially net n mineralization and ammonium consumption.

The study too analyzes the depolymerization of soil organic matter mediated by extracellular proteins, which controls the rate at which assimilable broken down organic matter is delivered. Transitory disturbances negatively impact the production, stability, and action of extracellular proteins, which are enthusiastically and nutritionally expensive and require microbial investment of C and nutrients. The study found diminished potential exercises of cellobiosidase,

chitinase, and phosphatase after both heat and freeze-thaw disturbances.

Prompt disturbance-induced increases in process rates are essentially driven by the accessibility and discharge of supplements from lysed microbial cells, whereas negative disturbance impacts are more likely to be caused by direct physical damage and physiological and structural changes of the microbial communities. The study observed a full recovery of almost all forms after 3 months, but for microbial P elements and hydrolytic enzyme activities, which remained considerably lower 3 months after disturbance.

The slow recovery of extracellular phosphatase activities and subsequently of P mineralization and microbial phosphate utilization rates over 3 months could have been caused by several mechanisms. First, the production of extracellular phosphatases seems have been down-regulated due to improved P accessibility inferred from disturbance-induced discharge of P from cell lysis. Second, a lower microbial P request due to slower development or diminished microbial biomass in focused microbial communities seem have driven to a lower generation of phosphatases relative to the undisturbed microbial communities.

Emerging Diseases

Climate alter may be a significant environmental indicator, with changes within the geological extend of species and territory disruptions bringing pathogens closer to individuals. Warming and precipitation changes have driven to the development of vectors such as mosquitoes, ticks, insects, birds, and mammals implicated in outbreaks by infections, microbes, animals, and protozoans. Territory disruptions caused by warming, dry season, heatwaves, fierce blazes, storms, surges, and land cover alter too bring pathogens closer to people.

Climatic dangers encourage contact between individuals and pathogens by moving people closer to pathogens. Heatwaves, for illustration, have been related with rising cases of waterborne infections such as *Vibrio*-associated contaminations, primary amoebic meningoencephalitis, and gastroenteritis. Storms, surges, and ocean level rise have caused human relocations implicated in cases of leptospirosis, cryptosporidiosis, Lassa fever, giardiasis, gastroenteritis, Legionnaires' infections, cholera, salmonellosis, shigellosis, pneumonia, typhoid, hepatitis, respiratory infection, and skin illnesses.

Climatic dangers moreover improve particular viewpoints of pathogens, counting progressed climate appropriateness for generation, increasing speed of the life cycle, expanding seasons/length of likely exposure, enhancing pathogen vector interactions, and increased virulence. Ocean warming and heavy precipitation provide fertile conditions for *Vibrio vulnificus* and *Vibrio cholerae*, driving to *Vibriosis* outbreaks in zones where this disease is rare.

Climatic risks have also decreased human capacity to manage with pathogens by modifying body condition, including stress from exposure to unsafe conditions, forcing individuals into risky conditions, harming foundation, constraining exposure to pathogens, and/or diminishing access to therapeutic care. Body malnutrition and condition influence immunocompetence to illness, and climate-driven changes can lead to decreased resistance to different illnesses. Climatic dangers also constrained individuals into risky circumstances that encouraged the hazard of disease

outbreaks (Mora *c et al.*, 2022) ^[9].

Adaptation and Resilience

Species abundance is regularly related with increased resistance and resilience of ecosystem capacities to beat irritations, to a great extent due to the protections theory. However, the robotic premise for these connections remains unclear, and numerous taxonomic and functional aspects of diversity may determine the resistance and flexibility of ecosystem functions in response to pulse perturbations such as climate extremes. Contrasts in species inclinations for environmental conditions, functional diversity, and dominant species traits are key factors in determining the resilience of ecosystems.

Soil microbial communities can direct their capacity to resist and recover from climate extremes through asynchrony of species responses, based on microbial life-history strategies related to resilience and speed of recovery. This asynchrony of species reactions is based on microbial life-history strategies related to tolerance to drying up and rapid development rate. Studies have appeared unique responses in population fluctuations and relative abundance of individual soil microbial taxa to climate extremes, demonstrating asynchronous microbial responses.

A few bacterial phyla can be differentiated into copiotrophic and oligotrophic strategies, with oligotrophs characterized by low growth rates and high resource utilize effectiveness being more resistant to climate extremes than copiotrophs.

The identification of broad life-history strategies related with resistance and flexibility in microbial responses to climate extremes has progressed our understanding of microbial responses. However, the particular microbial traits included remain unclear. The use of trait-based approaches in microbial biology is developing quickly, offering potential to identify subsets of microbial traits of significance for microbial life-history strategies related to resistance and versatility. For illustration, traits such as heterotrophic development methodology and dormancy potential have been connected to an improved ability of microbial-mediated functions to buffer perturbations. Genomic information, in conjunction with trait-based systems from plant ecology, could illuminate on the versatile strategies of dominant microbial taxa and their capacity to resist and recover from climate extremes. This can be particularly significant given that a relatively small subset of bacterial and fungal phylotypes rule soils universally, frequently being the strongest responders to drought.

Historical climate and soil properties can alter the intrinsic properties of soil microbial communities, affecting their capacity to resist and recover from climate extremes. Climate history can favor taxa with traits that empower them to buffer dry seasons or cause shifts within the physiology of person species due to adaptation or phenotypic versatility. Such shifts will influence the working of microbial communities in reaction to pulse perturbations such as dry-wet cycles. Soil abiotic properties, such as soil organic matter content and surface, can too alter the capacity of soil microbial communities to resist and recover from climate extremes.

Soil resource availability may play an critical part in altering microbial responses to climate extremes. A global meta-analysis uncovered that temporal variability or a lack of stability of soil microbial biomass was lower in soils of high

organic carbon and pH, proposing that these variables contribute to mitigation of stress and increase the steadiness of soil microbial communities. Microbial resilience to perturbations also seems more prominent in soils of high resource availability, which cultivates fast-growing microbial taxa with high rates of recovery from perturbations.

Plant community composition has been studied in limited detail, with most studies focusing on responses of aboveground plant communities. The essential mechanisms by which plants adjust microbial community responses to climate extremes are to a great extent indirect and work by changing the inborn qualities of microbial communities that confer resistance and versatility. Drought-induced shifts in vegetation phenology and composition, and vegetation mortality can moreover modify plant carbon exchange to soil organisms through changes in root turnover and plant litter.

Another component by which plants can adjust the reaction of soil life forms to climate extremes is through changing other outward variables, particularly soil dampness and nutrient accessibility. Understanding the supporting mechanisms that clarify such changeability and results for microbial resistance and strength to climate extremes may be a major challenge due to the multiyear or decadal timescale included.

Conclusion

Soil microbial communities play crucial roles in ecosystem functions and are highly sensitive to environmental changes, including temperature fluctuations, drought, flooding, metal toxicity, salinity, glacial retreat, and emerging diseases. These changes can impact microbial diversity, composition, and activity, consequently affecting nutrient cycling, soil fertility, and plant-microbe interactions. Climate change exacerbates these effects, with rising temperatures, ocean acidification, and other factors posing significant challenges. Understanding microbial responses to these stressors is essential for predicting ecosystem dynamics and informing adaptation strategies. However, more research is needed to fully grasp the intricate mechanisms driving microbial community resilience and adaptation to climate extremes (Rahman *et al.*, 2021) ^[1].

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Author's Contribution

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Conflict of Interest

Not available.

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