



Integrating free-living amoebae into climate-microbiome and One Health frameworks

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ABSTRACT

Climate change is altering microbial ecosystems at a global scale, yet the role of free-living amoebae within these shifting microbiomes remains incompletely understood. Free-living amoebae occupy soil, water, air, and built environments, where they contribute to microbial diversity, regulate nutrient cycling, and host diverse bacterial, fungal, and viral microorganisms. As temperature, moisture, and land-use patterns change, amoebal behaviour and their associated microbiomes may shift in ways that may affect soil fertility, water quality, microbial network stability, and the persistence of opportunistic pathogens. Through grazing, amoebae regulate bacterial turnover and mineral nutrient release from microbial biomass, providing a mechanistic link between nutrient cycling and plant accessible nutrient pools that underpin soil fertility. Understanding these dynamics is essential for planetary microbiome research and for strengthening One Health approaches that link environmental, animal, and human health. Herein, we discuss free-living amoebae in the context of climate change, the planetary microbiome, and One Health, and consider how their ecological roles may relate to broader shifts in microbial systems. We synthesise current evidence linking free-living amoebae to climate-responsive microbiome dynamics and propose their inclusion within planetary microbiome and One Health frameworks as responsive ecological indicators. Integrating amoebae into surveillance, ecological modelling, and climate-adaptation strategies may improve predictive capacity for tracking climate-driven microbial change.

1. Introduction

As global temperatures rise and ecosystems undergo change, understanding how microbial communities respond to environmental stress has become an increasing research priority (Tiedje et al., 2022). Free-living amoebae are ecologically diverse environmental protists that occur widely in soil, freshwater and built environments, where they contribute to microbial grazing, nutrient cycling and microbial community dynamics. Most free-living amoebae are not associated with human disease; however, several taxa, including *Acanthamoeba* spp., *Naegleria fowleri* and *Balamuthia mandrillaris*, are of particular clinical relevance. Here, we consider free-living amoebae broadly in relation to environmental and microbiome processes, while giving particular attention to clinically relevant taxa because of their One Health

significance. While bacteria, viruses and fungi have received considerable attention in climate-change research, comparatively little is known about how free-living amoebae respond to climate-driven environmental change or how such responses may influence microbial ecosystems and pathogen persistence (Balczun and Scheid, 2017; Anderson, 2018; Maciver et al., 2021; Robinson et al., 2025).

These ubiquitous environmental protists, including *Acanthamoeba*, *Naegleria fowleri*, and *Balamuthia mandrillaris*, are found in soil, freshwater, and man-made systems, where they function as microbial grazers and regulators of microbial diversity (Scheid, 2019; Mungroo et al., 2022). However, their ability to harbour, shelter, and in some cases amplify bacterial, fungal, and viral pathogens is a concern, due to the role of these environmental protists as both ecological stabilisers and potential public health threats (Proca-Ciobanu et al., 1975; reviewed in

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Siddiqui and Khan, 2012a). Their ecological importance is increasingly recognised, yet their role in climate-driven microbial change is under-recognised (Timmis et al., 2019).

There are major knowledge gaps in understanding how climate change is affecting the distribution, behaviour, and pathogenic potential of free-living amoebae (Maciver et al., 2020; Maciver et al., 2021). Throughout this review, “pathogenic” refers to free-living amoebae with recognised associations with human disease, whereas “non-pathogenic” refers to taxa without established clinical associations. These terms are used solely to describe clinical relevance and are not intended to imply distinct ecological characteristics or environmental responses. Unlike other microbial groups, such as the bacterial indicators *Escherichia coli*, *Legionella*, and enteric viruses, all of which are routinely monitored in water and clinical settings, pathogenic free-living amoebae are rarely included in standard surveillance programs, despite their presence in the same environments that are monitored (Standridge, 2008; Hull et al., 2019). While traditional indicators primarily reflect faecal contamination or acute failures in water quality, free-living amoebae provide complementary ecological information by integrating grazing activity, encystment responses and the persistence of intracellular microbial consortia. Their indicator value therefore lies in capturing broader microbial network changes that may not be detectable through bacterial or viral indicators alone. This has likely contributed to an underestimation of their importance in driving microbial interactions and facilitating the survival of pathogenic microorganisms under environmental stress. Their potential contribution to the persistence and dissemination of antimicrobial resistance, as well as their involvement in the emergence of novel pathogens, remains poorly characterised (Aslam and Aljasir, 2025). This omission has limited our understanding of how environmental change affects microbial interactions with disease relevance.

2. Literature search and review approach

Targeted searches were carried out of the peer-reviewed literature using combinations of terms related to free-living amoebae, climate change, environmental microbiology, microbiomes, One Health, soil and water ecology, pathogenicity, salinity, temperature and environmental stress. Relevant primary studies, reviews and conceptual papers were selected where they provided evidence on amoebal ecology, environmental responses, microbial interactions or implications for One Health and planetary microbiome frameworks. Particular emphasis was placed on studies addressing *Acanthamoeba*, *Naegleria*, *Balamuthia* and related free-living amoebae, while evidence from other protists was included where it provided relevant mechanistic or ecological context.

Climate-driven changes in temperature, precipitation, salinity, soil moisture, and ultraviolet radiation are likely to affect amoebic survival, encystment, and virulence through biologically plausible mechanisms, although direct empirical evidence remains limited (Classen et al., 2015). Yet empirical data in these areas remain scarce. The biological consequences of these shifts could be profound, not only in terms of microbial community dynamics but also in increasing human exposure to amoebae and their associated pathogens (Heilmann et al., 2024). Such environmental shifts may alter ecosystem functioning and increase human exposure through soil disturbance, aerosols, recreational waters, and urban water systems (Kellogg and Griffin, 2006). This could be particularly relevant in transitional environments such as coastal zones, urban water systems, and regions affected by extreme weather events.

Another overlooked area is the potential for pathogenic free-living amoebae to act as evolutionary incubators. Experimental evidence from another amoeba, *Dictyostelium discoideum*, shows that simulated warming can restructure amoeba–symbiont associations, leading to loss or altered stability of bacterial partners (Shu et al., 2020). Although this amoeba is free-living but not pathogenic, this model demonstrates that temperature shifts can directly influence amoeba–microbe symbioses, supporting the plausibility of similar climate-sensitive dynamics in environmental free-living amoebae (Das et al., 2023). By sheltering

microorganisms from harsh conditions, amoebae may facilitate horizontal gene transfer, promote microbial persistence, and contribute to the evolution of traits that enhance survival and virulence, although these mechanisms are biologically plausible, direct evidence demonstrating climate-driven evolutionary trajectories in free-living amoebae remains limited and warrants further investigation (Greub and Raoult, 2004; Siddiqui et al., 2022; Rayamajhee et al., 2022; Rayamajhee et al., 2024). These interactions are rarely considered in climate adaptation strategies or public health planning, and models that integrate pathogenic free-living amoebae into planetary health frameworks should be considered, as interactions may intensify under climate-driven environmental instability. Region-specific data on amoebic ecology across urban, agricultural, and natural ecosystems is also lacking.

To address these knowledge gaps, feasible experimental approaches include cross-sectional field surveys that relate amoebal abundance, cyst prevalence and intracellular microbiota to local temperature, moisture and land-use gradients, alongside laboratory climate-simulation systems that expose representative amoebae to controlled warming or drying to quantify shifts in encystment, grazing patterns and intracellular microbiomes. These could be feasible directions for testing the ideas outlined, which builds on prior work on free-living amoebae as opportunistic pathogens and microbial hosts. For example, coastal, arid or urban systems could be examined to relate amoebae species composition and cyst prevalence to seasonal temperature and precipitation patterns, while controlled climate simulation assays can be used to quantify how warming or drying influences encystment rates across representative taxa. Thus, coordinated and interdisciplinary research is urgently needed. Environmental microbiology, climate science, genomics, and epidemiology should converge to build a predictive understanding of how pathogenic free-living amoebae, and their microbial interactions are shaped by environmental change. Herein, we examine how free-living amoebae likely shape and respond to climate-sensitive microbial systems, discuss the implications for microbial network stability and disease emergence, and argue for their inclusion in predictive One Health and planetary microbiome frameworks. This will be essential in addressing microbial stability, evolutionary trajectories, and environmental–host interfaces in a warming world. In doing so, we advance the concept of free-living amoebae as sensitive indicators of climate-driven microbial change across soil, water, air and built environments.

3. Free-living amoebae and the ecosystem

Free-living amoebae are ubiquitous, and inhabit diverse environments: soil, dust, air, water and even extreme habitats such as Antarctica, forming a critical part of the microbial ecosystem (Rowbotham, 1980; De Jonckheere, 2006; Siddiqui et al., 2013; Salazar-Ardiles et al., 2022). Several species, including *Acanthamoeba* spp., *Naegleria fowleri*, *Balamuthia mandrillaris*, *Sappinia pedata*, *Vahlkampffia* spp., *Paravahlkampffia* spp. and *Vermamoeba* spp., are recognised as pathogenic and capable of causing opportunistic infections such as keratitis and fatal encephalitis (Visvesvara et al., 2007; Reyes-Batlle et al., 2017; Cope et al., 2020). Despite their wide distribution, to our knowledge, there are currently no global regulations addressing their presence in soil-based environments and standardized prevention or disinfection protocols are lacking. Importantly, these ecological functions are not restricted to species recognised as pathogenic. While pathogenic free-living amoebae are of particular clinical interest, both pathogenic and non-pathogenic species contribute to microbial grazing, nutrient cycling, and ecosystem functioning, and their ecological roles should not be inferred solely from their clinical relevance.

Soil is an ideal habitat for amoebae due to its rich supply of nutrients and complex microbial communities on which they feed (Denet et al., 2017). Their diet includes bacteria, fungi, protists and organic matter, making them essential regulators of soil microbial populations and nutrient cycling. In particular, amoebae such as *Acanthamoeba* act as dominant bacterial grazers responsible for a significant proportion of

bacterial reduction in soil ecosystems (Sinclair et al., 1981). By consuming primary decomposers like bacteria and releasing mineral nutrients sequestered within bacterial biomass, they act as secondary decomposers enhancing the availability of carbon, nitrogen and phosphorus to other organisms (Elliott et al., 1979; Clarholm, 1981; Clarholm, 2002; Rønn et al., 2002).

The interactions between *Acanthamoeba* and bacteria illustrate this process. Soils containing both showed significantly greater mineralization of key nutrients compared to soils with bacteria alone (Rosenberg et al., 2009). These dynamics also impact plant systems; experiments in the rhizosphere of *Arabidopsis thaliana* showed that grazing by *Acanthamoeba* altered bacterial community composition and promoted plant growth (Rosenberg et al., 2009). Mechanistically, amoebal grazing shifts bacterial community composition and accelerates nutrient mineralization, increasing or redistributing plant available nitrogen and phosphorus, which links microbial turnover to soil fertility and carbon cycling. Comparable high-organic environments such as wetlands, bogs, and estuarine sediments, where plant cover, root architecture, and hydrological mixing structure microhabitats, are likewise expected to support abundant amoebal communities. Vegetation-driven oxygen gradients, organic-matter inputs, and localised redox niches in these systems shape microbial activity and nutrient turnover (Mitsch and Gosselink, 2015), while plant cover in peatlands and wetland soils is known to influence microbial enzyme activity and carbon release dynamics (Freeman et al., 2001). These factors together create microbially rich interfaces where free-living amoebae are likely to be persistent and ecologically influential. Comparable processes also occur in forest ecosystems, where leaf-litter layers and fungal-rich horizons form highly active microbial interfaces that support protist grazing and decomposition processes (Boddy, 1993). As nutrient cycling is climate-sensitive, shifts in amoebal behaviour under warming conditions may alter soil fertility, carbon turnover, and microbial succession.

Beyond nutrient cycling, these protists also play a role in microbial interactions relevant to human health. Many bacterial species have evolved mechanisms to survive amoebal digestion and persist within both trophozoite and cyst stages (Cirillo et al., 1999; Greub and Raoult, 2004). The highly resilient cysts enable free-living amoebae and their internalized bacteria to withstand desiccation, temperature fluctuations, chemicals and standard disinfection procedures, potentially facilitating the entry of pathogenic bacteria into human-related environments (Aksozek et al., 2002; Siddiqui et al., 2013; Siddiqui et al., 2008). Experimental studies have shown that *Acanthamoeba* cysts can survive exposure to extreme desiccation, ultraviolet radiation, and common disinfectants for prolonged periods, demonstrating a level of environmental persistence that exceeds that of many free-living bacteria (Aksozek et al., 2002). The life cycle of amoebae, which includes an active trophozoite and a dormant cyst stage and a temporary flagellate stage in species such as *Naegleria fowleri*, reinforces both their ecological persistence and their role as reservoirs for pathogens (Rodríguez-Zaragoza, 1994; Stahl and Olson, 2021). This combination of environmental resilience and ecological importance highlights the need for deeper understanding of their dynamics in soil ecosystems. Recent work in soil microbial ecology has shown that protist driven grazing can enhance litter decomposition and increase microbial carbon flux, with these effects varying according to temperature, indicating that protist activity responds to climate relevant shifts and can influence carbon cycling processes within soil microbiomes (Geisen et al., 2021).

Thus, free-living amoebae represent critical nodes in environmental microbial networks, influencing both the diversity and functional potential of surrounding communities. Their ability to host, protect, and redistribute microorganisms reflects the ecological interactions that likely sustain the broader ecosystems. Environmental disturbances that affect amoebal populations, including temperature fluctuations, salinity changes, or pollution, may propagate through microbial food webs and alter the stability and resilience of the ecosystem. These local microbial imbalances are increasingly being recognised as integral elements of the

wider planetary microbiome, in turn with such environmental perturbations influencing soil health, water quality, and ultimately human and animal well-being. These relationships highlight that all components of the biosphere are connected, and that microbial ecology forms a vital link between environmental processes and planetary health. Overlooking the role of free-living amoebae within these systems risks neglecting a key element of microbial connectivity and ecosystem resilience. These ecological functions position free-living amoebae as sensitive components of environmental homeostasis, making their responses to climate change particularly consequential.

4. One Health and the planetary microbiome

Human and planetary health are fundamentally interconnected, with microbial ecosystems, particularly those found in soil, providing the foundation for both (van Bruggen et al., 2019). The One Health framework recognises that the health of humans, animals, plants, and the environment forms a single, integrated system governed by microbial processes (Zinsstag et al., 2011; Pitt and Gunn, 2024; Adisasmito et al., 2022). Although originally focused on zoonoses, antimicrobial resistance, and vector ecology, this framework has increasingly expanded to include microbial communities as essential components of ecosystem and host health (Carlson et al., 2022; Banerjee and Van Der Heijden, 2023). The planetary microbiome refers to the interconnected microbial systems across soil, water, air, and host organisms that collectively influence planetary processes (Timmis and Ramos, 2021; van Bruggen et al., 2019).

Within this context, free-living amoebae represent an important yet often overlooked element of the planetary microbiome. Their ubiquitous presence across soil, water, and air environments exemplifies the microbial continuity that emphasizes One Health. As active grazers, hosts, and reservoirs for a range of microorganisms, amoebae influence nutrient cycling, pathogen dynamics, and ecosystem resilience, bridging environmental and host-associated microbiomes. Their interactions with bacteria, fungi, and viruses reflect the same ecological principles that operate at larger scales, where environmental disturbance can ripple across biological and health systems.

The planetary microbiome, encompassing soil, water, air, and host-associated microbial systems, thus functions as an invisible yet essential infrastructure that supports life, regulates disease, and sustains ecological balance (Timmis and Ramos, 2021). Soils are a cornerstone of this framework, acting as vast reservoirs of microbial diversity and sources of both beneficial and pathogenic microorganisms (Roslund et al., 2024). The soil microbiome contributes directly and indirectly to plant, animal, and human health, and growing evidence indicates that many microorganisms, including those associated with amoebae, are shared across these domains (van Bruggen et al., 2019).

This interconnectedness underscores the concept of a planetary microbiome, which emphasizes the microbial links between ecosystems and the inseparability of environmental and biological health. Ignoring the ecological role of free-living amoebae within this continuum risks overlooking a key component of microbial communication and planetary resilience. Within this planetary microbiome, free-living amoebae (both pathogenic and non-pathogenic) occupy a crucial but often underappreciated position. These microbial predators are key players in soil and aquatic microbiomes, shaping microbial diversity through their grazing activity and influencing biogeochemical cycles (Rodríguez-Zaragoza, 1994; Siddiqui and Khan, 2012b.). Their ecological roles extend beyond microbial regulation; amoebae interact with bacteria, fungi, and viruses, and can serve as reservoirs and vectors for opportunistic human pathogens. Species such as *Acanthamoeba*, *Naegleria fowleri*, and *Balamuthia mandrillaris* highlight the intersection of environmental microbiology with clinical relevance, particularly in vulnerable or changing environments (Scheid, 2019; Mungroo et al., 2022).

Global environmental change, particularly climate change, may be

reshaping microbial ecosystems (Tiedje et al., 2022). Rising temperatures, altered precipitation patterns, and anthropogenic land use may be shifting the distribution and behaviour of free-living amoebae and their associated microbiomes. These changes may favour the proliferation of pathogenic strains, increase human exposure through water and soil contact, and may cause disturbances to the microbial equilibrium critical to both ecosystem and host resilience (Maciver et al., 2021). This state of global microbial dysbiosis is likely to have implications for the emergence and transmission of disease and demands attention within One Health and planetary health strategies. Climate-linked shifts in microbial communities are increasingly being recognised as contributing to the emergence and re-emergence of infectious diseases, as seen in recent patterns of monkeypox, *Vibrio* outbreaks, and vector-borne infections in new regions (Baker-Austin et al., 2017). Although these pathogens may not be directly related to free-living amoebae, they illustrate how environmental instability may reshape host-microbe interactions and alter disease landscapes. Importantly, free-living amoebae themselves can harbour, protect, and transport a wide range of bacterial, fungal, and viral pathogens, meaning that climate-driven changes in amoebal ecology may have wider implications for pathogen persistence and environmental transmission (Mungroo et al., 2022; Siddiqui et al., 2023).

Recently, the planetary boundaries framework has identified nine key Earth system processes, including climate change, biosphere integrity, and biogeochemical flows, that must remain within safe limits to maintain a stable and resilient planet, highlighting the scale of anthropogenic impact on environmental and microbial health (Richardson et al., 2023; van Vuuren et al., 2025). The role of free-living amoebae within these processes also needs to be understood. Despite their ubiquity and ecological influence, free-living amoebae remain largely absent from One Health models, creating a significant gap in understanding how microbial processes respond to environmental change. In practical terms, incorporating free-living amoebae into One Health frameworks could involve monitoring indicators such as amoebal abundance, trophozoite-to-cyst ratios, species diversity, and the prevalence of intracellular microorganisms alongside environmental variables including temperature, moisture, salinity, and land-use change. Linking these environmental measurements with water-quality surveillance, environmental monitoring, and human disease reporting could improve understanding of how climate-driven changes in microbial ecosystems influence pathogen persistence, exposure pathways, and public health risk. Although these relationships require further validation, such integrated surveillance would provide a practical framework for evaluating environmental, animal, and human health within a One Health context.

5. Climate change and microbiomes

Climate change is reshaping microbial ecosystems at every scale and understanding how free-living amoebae interact with the broader planetary microbiome is central to predicting these shifts (Cavicchioli et al., 2019). At the environmental scale, this includes shifts in atmospheric gaseous composition, temperature, pressure, relative humidity and weather patterns, changes in depth-related temperature structure, salinity and circulation in open marine systems, and altered flow regimes, stratification, salinity and mixing in rivers, lakes, wetlands and coastal or estuarine zones. Temperature increases, altered hydrological cycles, soil degradation, nutrient imbalance, and extreme weather events are transforming microbial communities worldwide. Within this context, free-living amoebae serve as both ecological stabilisers and amplifiers, influencing the structure, diversity, and resilience of microbial networks in soil, water, and air. Their behaviour, abundance, and interactions therefore provide an early indication of how climate-driven disturbances ripple through microbial ecosystems.

At the organismal level, climate-sensitive environmental drivers are translated into changes in protist physiology and biochemistry. In *Acanthamoeba*, temperature-dependent adjustments in fatty-acid

metabolism and membrane composition affect cell division, oxygen uptake, phagocytic activity and plasma-membrane fluidity (Avery et al., 1994; Avery et al., 1995). In *Giardia*, shifts in lipid and sterol composition across trophozoite and encysting stages, together with altered desaturase activity, illustrate how environmental conditions shape membrane properties and life-cycle progression (Jarroll et al., 1981; Ellis et al., 1996). Membrane-potential measurements in *Giardia* further demonstrate links between ionic gradients, energetics and responses to external stressors (Biagini et al., 2000). More broadly, experimental work on circadian and ultradian clock-controlled rhythms in unicellular microorganisms shows that temporal organisation of metabolism and behaviour is itself sensitive to temperature and other external cues (Lloyd, 1997; Jenkins et al., 2025). Collectively, these studies support a mechanistic pathway by which climate-linked changes in temperature and chemistry may modulate growth, motility, membrane function and rhythmic behaviour in protists, including free-living amoebae.

Free-living amoebae respond rapidly to changes in moisture, temperature, and nutrient availability, making them sensitive indicators of environmental instability. Their ability to transition between trophozoite, cyst, and in some species flagellate stages allows them to persist during drought, heat waves, and chemical stress. These adaptive traits, combined with their role as microbial grazers, place them at the centre of shifting microbial food webs. As climate pressures intensify, amoebae may drive shifts in microbial composition by selectively grazing on some groups while protecting others that survive intracellularly. Salinity represents an additional climate-sensitive driver of amoebal ecology, particularly in coastal systems and regions affected by seawater intrusion or water reuse. Experimental evidence demonstrates species-specific tolerance patterns among pathogenic free-living amoebae. For example, experimental exposure to increasing salinity reduced trophozoite growth of *N. fowleri* and *A. griffini*. In saline-water experiments, 34 g/L marine salt, used to approximate seawater-level salinity, markedly inhibited trophozoite growth, while parallel culture-medium experiments examined comparable NaCl concentrations (Arberas-Jiménez et al., 2024). These findings suggest that salinity shifts may restructure amoebal community composition, selectively favouring tolerant taxa and indirectly altering associated bacterial networks. In the context of climate-driven coastal change, altered precipitation regimes and saline intrusion may therefore influence both amoebal distribution and pathogen persistence in water systems.

Moreover, many microorganisms that resist amoebal digestion possess traits that enhance survival under environmental stress, including antimicrobial resistance, increased biofilm formation, and improved tolerance to desiccation and temperature fluctuations. Climate change may therefore inadvertently favour microorganisms that are pre-adapted to both amoebal predation and human infection. This introduces an important but often overlooked link between environmental change and the emergence of pathogenic or opportunistic microbes.

Because amoebae act as reservoirs for bacteria, fungi, and viruses, climate-driven alterations in amoebal ecology may influence the persistence and dissemination of microbial pathogens in natural and built environments. In addition to direct environmental effects, climate-driven changes in microbial prey and intracellular microorganisms may also indirectly influence the persistence and behaviour of pathogenic free-living amoebae, although these interactions remain poorly understood and warrant further investigation. In this context, sensitive indicators refer to measurable shifts in amoebal abundance, trophozoite to cyst ratios and associated intracellular microbiota that respond rapidly to climate relevant perturbations and can therefore reflect broader microbial community change. Rising temperatures may expand the geographic range of species such as *Naegleria fowleri*, while fluctuating moisture conditions may alter the behaviour of *Acanthamoeba* spp. and *Balamuthia mandrillaris* in soil and dust, although evidence directly demonstrating climate-driven range expansion remains limited. Increased urbanisation, water reuse, and stressed infrastructure could

further amplify human exposure pathways through aerosols, soil disturbance, and domestic water systems. Predicting the long-term ecological responses of free-living amoebae to climate change remains challenging. Responses are likely to vary among species and ecosystems, with some taxa potentially benefiting from environmental change while others may decline or be outcompeted. For example, tropical systems with consistently warm temperatures and year-round moisture may support more continuous amoebal activity with less pronounced seasonal fluctuation, whereas temperate regions may show stronger seasonal shifts linked to temperature and moisture availability. Coastal and arid regions may differ further, with salinity changes, episodic rainfall and prolonged drying exerting distinct selective pressures on amoebal survival, encystment and community composition. Consequently, regional variation should be considered when evaluating free-living amoebae as climate-responsive indicators.

Taken together, these interactions make free-living amoebae a powerful lens for examining how microscopic ecological processes scale up to affect planetary health. They highlight the need to incorporate microbial predators and their associated microbiomes into models of climate resilience, disease emergence, and ecosystem stability. Integrating amoebae into the climate-microbiome narrative provides mechanistic insight into how environmental disruption can destabilise microbial equilibria and influence health outcomes across species and ecosystems. Climate-sensitive drivers including warming, altered precipitation, salinity fluctuation, ultraviolet radiation, nutrient enrichment, land-use change, and extreme weather events may influence amoebal trophozoite activity, encystment dynamics, and community composition. These shifts may in turn modify microbial grazing pressure, intracellular pathogen persistence, and broader network structure across soil and aquatic systems. Such pathways are best viewed as ecologically plausible interactions rather than direct causal chains, as outcomes will be mediated by local factors including soil structure, hydrology, and environmental disturbance intensity.

6. Recommendations for One Health and planetary microbiome research

Free-living amoebae should be incorporated into environmental, ecological, and public-health frameworks that aim to understand and mitigate the impacts of climate change on microbial systems. Their ubiquity, ecological importance, and capacity to harbour diverse intracellular microorganisms make them essential indicators of ecosystem stability. Incorporating *Acanthamoeba* spp., *Naegleria fowleri*, and *Balamuthia mandrillaris* into routine soil and water surveillance would strengthen early detection of microbial shifts, particularly in regions undergoing rapid climatic, hydrological, or land-use change. Surveillance programmes that already monitor bacterial and viral indicators could be expanded to include amoebae, capturing a broader spectrum of microbial interactions relevant to environmental and human health. Routine surveillance of free-living amoebae will require reliable detection strategies. Conventional microscopy remains a practical and cost-effective first-line method for detecting trophozoites and cysts; however, it is labour-intensive, dependent on operator expertise, and has limited taxonomic resolution. In contrast, molecular methods, including PCR and quantitative PCR (qPCR), provide greater sensitivity and specificity for species identification and environmental surveillance, enabling the detection of low-abundance amoebae and facilitating rapid monitoring of pathogenic species. Recent advances, including nanoparticle-assisted PCR approaches, have further improved assay performance and detection efficiency (Gabriel et al., 2018; Rasheed et al., 2020; Siddiqui et al., 2025). From a resource perspective, microscopy has relatively low consumable costs but requires trained personnel and substantial hands-on time, whereas targeted PCR/qPCR can generally use the same extraction, amplification and quality-control infrastructure already employed for bacterial and viral surveillance, limiting additional capital requirements in equipped laboratories. In

contrast, metagenomic approaches require greater sequencing, bioinformatics and data-storage resources and may therefore be more appropriate for targeted research or reference-laboratory surveillance than routine first-line monitoring. Nevertheless, assay standardisation and validation across different environmental matrices remain important challenges. Initial standardisation efforts could prioritise matrices of major One Health relevance, including freshwater and drinking-water systems, coastal waters and agricultural or urban soils. Inter-laboratory validation could use harmonised sampling and extraction protocols, shared reference materials and blinded panels to compare analytical sensitivity, specificity, reproducibility and recovery across laboratories. Establishing baseline abundances of free-living amoebae across diverse environmental systems will be essential for distinguishing natural ecological variation from climate-driven changes in distribution and abundance. Importantly, surveillance of free-living amoebae should complement, rather than replace, existing bacterial and viral monitoring programmes, providing additional ecological insight into microbial interactions and pathogen persistence. Over time, insights from such monitoring could also inform the development of biosensor-based early warning tools for climate-sensitive microbial hazards, particularly in water and soil systems (Williams et al., 2024). Implementation challenges should also be recognised. Routine inclusion of free-living amoebae in environmental surveillance will require consideration of laboratory capacity, methodological standardisation, personnel training, sampling frequency and additional analytical costs. A phased approach may therefore be most practical, beginning with targeted surveillance in climate-sensitive or high-risk environments, followed by inter-laboratory validation and expansion into routine monitoring where evidence demonstrates added value alongside existing bacterial and viral indicators.

To build predictive capacity, interdisciplinary research is needed to quantify how climate-sensitive variables such as temperature, moisture, salinity, nutrient flux, and ultraviolet radiation shape amoebal behaviour and their interactions with bacteria, fungi, and viruses. In agricultural soils, fertiliser application and pH adjustment through liming act as additional land-management pressures that modify microbial community structure and functional gene abundances, interacting with climate-sensitive variables to influence amoebal habitats (Madegwa and Uchida, 2021). Experimental systems that simulate future climate scenarios would allow researchers to explore how amoebae influence microbial succession, biogeochemical cycling, and the persistence of opportunistic pathogens. Genomic, transcriptomic, and metagenomic approaches should be applied to characterise intracellular microbial consortia within amoebae and to determine how climate pressures modify these associations, including the potential for horizontal gene transfer and the emergence of antimicrobial resistance. In practical terms, monitoring efforts could prioritise representative taxa such as *Acanthamoeba*, *Naegleria* and *Balamuthia*, together with their intracellular microbiota. Useful metrics include relative abundance, cyst prevalence and detectable intracellular bacteria. Feasible detection approaches include microscopy with molecular confirmation, targeted qPCR for key taxa and metagenomic screening where possible. Sampling could be conducted seasonally in coastal, urban water and agricultural soils to capture climate linked fluctuations, with higher frequency in regions undergoing rapid hydrological or land use change. These examples illustrate potential options rather than fixed protocols and are intended to guide future applied work.

Environmental agencies and policymakers should recognise that free-living amoebae respond rapidly to environmental disturbance and can provide early insight into deteriorating soil quality, stressed freshwater systems, or compromised water infrastructure (Aslam and Aljasir, 2025). Integrating amoebae into climate-adaptation and water-safety frameworks would enhance preparedness for microbial hazards associated with warming temperatures, water scarcity, and extreme weather events. This approach aligns with planetary-health priorities that emphasise ecosystem resilience, biodiversity protection, and sustainable

stewardship of natural resources.

Cross-sector collaboration is essential for progressing these efforts. Environmental scientists, microbiologists, clinicians, climate scientists, and public-health authorities should work together to embed amoebae into predictive ecological models and risk assessments. Linking environmental monitoring with public-health reporting systems will help identify potential exposure pathways and emerging vulnerabilities. At a broader scale, incorporating amoebae into the planetary microbiome concept will deepen understanding of how microscopic ecological processes influence macroscopic outcomes, including agricultural productivity, water security, and infectious-disease emergence.

7. Concluding remarks

Climate change is transforming microbial ecosystems in ways that remain only partially understood, and free-living amoebae represent a crucial but long-neglected component of this picture. Their widespread presence across soil, water, and air, together with their dual roles as microbial regulators and hosts for diverse intracellular organisms, positions them at the centre of climate-sensitive microbial networks. As environmental conditions shift, the behaviour, distribution, and microbial associations of amoebae are likely to change in parallel, with implications for nutrient cycling, soil and water quality, microbial community structure, and the persistence of opportunistic pathogens. These dynamics underscore the need to incorporate amoebae into climate-microbiome research, where they can provide mechanistic insight into how microscopic interactions scale to influence broader ecological resilience.

Recognising free-living amoebae within One Health and planetary microbiome frameworks will help bridge gaps between environmental science, microbial ecology, and public health. Their responses to temperature, moisture, and land-use pressures offer a valuable lens through which to interpret environmental instability and anticipate downstream biological consequences. Integrating amoebae into surveillance programmes, predictive models, and climate-adaptation strategies will enhance our understanding of microbial change in a warming world and improve our capacity to identify emerging risks. As planetary systems continue to be reshaped by anthropogenic pressures, acknowledging the ecological significance of amoebae will contribute to a more complete and resilient approach to safeguarding environmental, animal, and human health. We propose that incorporating free-living amoebae into planetary microbiome and One Health models offers a novel lens, as a potential practical indicator system for tracking microbial responses to climate change.

Consent to participate and consent for publication

Not applicable.

Authors contribution

NAK and RS envisioned the concept amid discussions with SM and DL. RS reviewed literature and prepared the first draft of the manuscript together with NAK, SM and DL. All authors reviewed and approved the final manuscript.

CRedit authorship contribution statement

Ruqaiyyah Siddiqui: Writing – original draft, Resources, Investigation, Data curation, Conceptualization. **Sutherland K. Maciver:** Writing – review & editing, Supervision, Investigation, Formal analysis, Conceptualization. **David Lloyd:** Writing – review & editing, Supervision, Investigation, Conceptualization. **Naveed Ahmed Khan:** Writing – original draft, Supervision, Resources, Project administration, Investigation, Formal analysis, Conceptualization.

Ethical approval

Not applicable.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Data availability

No data was used for the research described in the article.

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