



Reframing antimicrobial resistance as a land-system challenge through environmental pathways and climate interactions



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Antimicrobial resistance (AMR) is a planetary health challenge, yet land-system change remains overlooked. This review examines how agriculture, urbanisation, waste management, deforestation, aquaculture and climate-driven transitions shape resistance through altered input intensity, habitat reorganisation and enhanced connectivity. It identifies evidence gaps across vulnerable settings and proposes pathway-based surveillance, integrated datasets, longitudinal studies and coordinated interventions to reduce resistance selection, persistence and transmission across connected landscapes, informing research, policy and implementation.

AMR is usually framed as the consequence of antimicrobial use in human and veterinary medicine, with policy responses focused on stewardship, diagnostics, infection prevention and pharmaceutical innovation¹. That framing is necessary but incomplete since resistance is also shaped by ecological disturbance, land-use decisions, environmental contamination and the material circulation of organisms, genetic material, and chemicals across landscapes. As a result, AMR can no longer be treated solely as a biomedical externality. Land use sits at the centre of the problem, shaping and reinforcing a set of interconnected challenges spanning patterns of development, pressures on waste management systems, persistent gaps in pollution and chemicals governance, and the effectiveness of climate adaptation.

This framing aligns closely with the planetary boundaries agenda^{2,3}. Land-system change is one of the Earth system processes through which human activity reorganises the biosphere³. It is inseparable from climate change, freshwater change, novel entities, and biodiversity loss. For AMR, land-system change matters because it determines where people farm, where cities expand, how waste is produced and recycled, how livestock are kept, where wetlands are drained or restored, and where crops thrive or fail. In doing so, it shapes the physical and ecological settings in which bacteria, fungi and other microorganisms encounter antimicrobial drugs, including

antibiotics, antifungals and antiparasitics. It also affects exposure to non-antimicrobial selective pressures, including biocides, pesticides, metals, and other environmental stressors. As climate change intensifies, land-system change increasingly interacts with adaptation responses, altering how water, soils, crops, livestock, and waste systems are managed, and how AMR risks are distributed. In other words, land-system change governs the contexts in which resistance is selected, maintained and transmitted.

This narrative review and conceptual synthesis was developed by the Land-Systems Change Working Group of CLIMAR, a Biotechnology and Biological Sciences Research Council (BBSRC)-funded network examining the intersection of climate change and antimicrobial resistance (AMR) through a planetary health framework. Integrating multidisciplinary expertise across environmental microbiology, veterinary and human medicine, geography, soil science, wastewater management, aquaculture, climate adaptation, biodiversity, and policy, we synthesise current evidence on how land-system alterations drive environmental AMR pathways. Furthermore, we identify critical priorities for surveillance, targeted intervention, and environmental governance. Emphasis is placed on high-risk and unstable contexts, including rapid urbanisation, informal settlements, and conflict-affected or environmentally disrupted settings, as well as ecological vectors such as aquaculture and wildlife-mediated connectivity.

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The Land-System Framework of Antimicrobial Resistance (AMR)

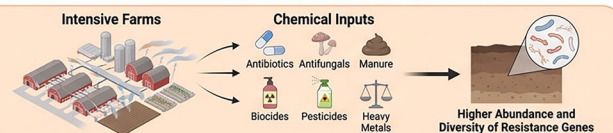
AMR as a Land-Use Problem

Beyond medicine, AMR is shaped by ecological disturbance, land use decisions, and the material circulation of organisms across landscapes.

Land-System Change

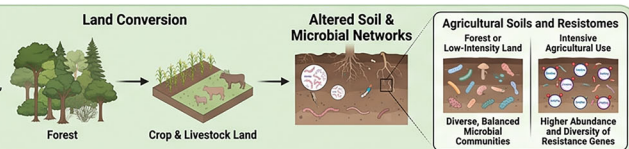
1. Altered Input Intensity

Land use transitions change the volume and geography of chemical inputs, including antibiotics, antifungals, manure, biocides, pesticides, and heavy metals.



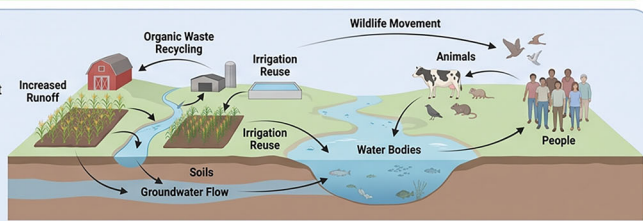
2. Habitat Reorganisation

Converting land (e.g., forest to crop) alters soil parameters, biodiversity, and microbial networks, creating conditions that favour the persistence of mobile genetic elements and resistance genes.



3. Enhanced Connectivity

Increased runoff, organic waste recycling, irrigation reuse, and wildlife movement create efficient pathways that connect soils, water, animals, and people.



Planetary Boundary Interaction

Land system change interacts with climate change, freshwater change, and biodiversity loss to govern the contexts in which resistance is selected and transmitted.



Half of Habitable Land is Agricultural



Global food systems, particularly intensive livestock production, generate concentrated waste streams and antimicrobial dependence that impact soil and water health.

Environmental pathways and hotspots

Rapid Urbanisation and Informal Settlements



Inadequate Sanitation
Concentration of Pharmaceutical and Industrial Residues
Structural Sorption
Structurally Produced Risk

Climate-driven transitions



Climate Stress
Antimicrobial-Intensive Livestock
Local Geography of Manure and Pathogens

Wildlife as landscape vectors



Scavenging species
Gulls and Wildfowl
Moving Resistant Organisms Across Regions
Polluted Environments (Landfills, Wastewater)
Remote or Agricultural Settings

Fig. 1 | Conceptual framework linking land-system change to antimicrobial resistance within a planetary health context. Land-system change shapes environmental AMR risk through three interconnected mechanisms: altered input intensity, habitat reorganisation and enhanced connectivity. Altered input intensity changes the volume, composition and spatial distribution of antimicrobials, manure, sewage sludge, biocides, pesticides, metals and other co-selective contaminants. Habitat reorganisation modifies soil, water and built environments by changing hydrology, chemistry, biodiversity, host density and microbial community structure, creating conditions that may favour persistence, selection and genetic exchange.

Enhanced connectivity increases the movement of resistant organisms, antimicrobial resistance genes and mobile genetic elements across soils, waters, animals, wildlife and human populations through runoff, drainage, irrigation, organic waste recycling, wastewater discharge, trade and movement. The framework extends One Health approaches by situating AMR within broader interactions among land use, climate change, pollution, biodiversity, infrastructure and governance. Figure created in BioRender. Read, D. (2026) <https://BioRender.com/slzzg0e>.

Ultimately, we underscore the critical necessity of explicitly integrating spatial land-use datasets into robust AMR surveillance frameworks.

Conceptual framework for how land-system change drives AMR

Numerous reviews and international assessments have established that environmental reservoirs, selective environments and transmission pathways are integral to the emergence and dissemination of AMR^{4–6}. The distinctive focus of this review is therefore not simply to reiterate the environmental dimension of AMR, but to examine how land-system change structures that dimension. Land-system change reorganises terrestrial and aquatic environments and interacts with other Earth-system pressures, including climate change, freshwater change, pollution and biodiversity loss^{2,3}. Drawing on the literature reviewed within this review, we propose a simple framework in which land-system change affects AMR through three linked mechanisms, *i.e.* altered input intensity, habitat reorganisation and enhanced connectivity. This framework builds on One Health approaches by recognising the connections between human, animal and environmental health^{4,5}, but extends the framing through a planetary health lens by foregrounding land use, climate change, pollution, biodiversity loss and infrastructure as conditions that shape AMR selection, persistence and transmission (Fig. 1). The first mechanism is altered input intensity. Land-use change often alters the extent to which environmental pollutants are introduced. These include, but are not limited to antibiotics, antifungals, manure, sewage sludge, biosolids, biocides, pesticides or metals. For example, intensification of livestock systems increases total waste loading and often increases antimicrobial exposure^{7,8}, while some forms of urban expansion increase pharmaceutical and detergent loads to wastewater and receiving waters^{9,10}. The second mechanism is habitat reorganisation.

Conversion of forests to cropland, cropland to pasture, peri-urban land to settlements, or low-intensity farming to intensive agricultural production changes soil chemical, physical and biological parameters, hydrology, biodiversity, microbial network structure and host density. Protists are likely to play an important but under-recognised role within these reorganised habitats by mediating microbial encounter rates, selectively removing susceptible bacterial populations, and enriching for phenotypes associated with intracellular persistence, stress tolerance, and AMR^{11,12}. These habitat changes may favour the persistence and exchange of antimicrobial resistance genes (ARGs), which are genes that allow microorganisms to survive exposure to antimicrobial drugs. They may also increase the movement of mobile genetic elements, which are segments of DNA that can move within and between microorganisms, helping resistance traits spread between bacteria and other microbes. As a result, land-use change can create environmental conditions that favour the persistence of resistant microorganisms and resistance determinants, while also altering the survival and dissemination of potential pathogens⁵. The third mechanism is enhanced connectivity. As land and water systems become increasingly connected through runoff, artificial drainage, land application of organic wastes, irrigation with reclaimed wastewater, wildlife movement, trade and transport, resistant organisms and resistance genes can move more readily across environmental compartments. However, the extent to which these flows translate into AMR risk, *i.e.* increased mobilisation, dissemination and potential exposure to ARGs, depends on waste-treatment efficacy, manure and slurry management, biosolids processing, drainage infrastructure, regulatory controls and monitoring capacity, which together shape the attenuation, mobilisation, and dissemination of resistance across landscapes.

Aerial transport represents an additional and comparatively under-recognised component of enhanced connectivity. Resistant microorganisms, ARGs and microbial particles can become aerosolised from livestock housing and manure, agricultural soils, wastewater treatment and sludge handling, composting and biowaste facilities, and other urban and industrial sources. Atmospheric transport can subsequently move these biological materials beyond their point of origin, while deposition can reconnect airborne AMR with soils, vegetation and surface waters. Air therefore represents not simply another environmental reservoir, but a pathway linking land-use activities and waste systems across spatial scales. The magnitude and distance of dispersal are likely to depend on source characteristics, particle size, meteorology, vegetation cover and landscape structure, while inhalation provides a potential direct exposure route for humans and animals. Climate change and climate adaptation intersect with all three mechanisms. Intensification or waste reuse as adaptation strategies can increase input pressures while hydrological extremes can alter the connectivity of soils, waters, and waste systems. Subsequently, longer-term land shifts can reorganise microbial habitats and host interfaces. Climate therefore acts both directly on environmental conditions relevant to AMR selection and indirectly through land-use decisions that shape where exposures occur. This framework helps move the discussion beyond static descriptions of AMR in one compartment. It also explains why land-system change is particularly relevant to the environmental dimension of AMR. The environment is not merely a passive sink for residues and resistant organisms; it is an active arena of selection, persistence, recombination, and redistribution. The significance of this for policy is that interventions targeted at one node, such as prescribing, are likely to be most effective when complemented by measures that reduce the selection, mobilisation, and recycling of resistance determinants across connected landscapes.

Land-system change in the planetary boundaries context

Land-system change is not the most transgressed boundary in the current planetary boundaries assessment, but it remains under substantial pressure and has important interactions with other boundaries³. Global land-use synthesis shows that approximately half of the world's habitable land is used for agriculture^{13,14}. Moreover, the global food system remains highly uneven in land efficiency. For example, livestock uses more than three-quarters of global agricultural land while providing a much smaller share of calories than its footprint suggests^{14,15}. However, a substantial proportion of this land comprises permanent pasture or rangeland that is unsuitable or only marginally suitable for crop production. This qualification does not remove the land-system implications of livestock production but highlights that land-use efficiency should be interpreted in relation to land quality, feed sourcing, and the distinction between grazing land and cropland used for animal feed. Nevertheless, the land demands associated with livestock production remain relevant to both climate and AMR because expansion of pasture and feed production contributes to deforestation and greenhouse gas emissions, while intensification of animal production can generate concentrated waste streams, increase infectious disease risks and create conditions associated with inappropriate antimicrobial use.

Food system restructuring is also policy-relevant because crop failure under climate stress may encourage shifts towards livestock systems in some settings and displace feed production elsewhere¹⁶. This is not merely a question of food security since it changes the geography of manure, slurry, runoff, veterinary drug use, biosecurity risk, and pathogen exposure. The land-system perspective therefore allows AMR to be analysed alongside climate mitigation, food system resilience, and biodiversity policy, rather than as a narrow public health endpoint.

Agricultural intensification, soils and resistomes

Agricultural soils are among the best-established environmental reservoirs of AMR¹⁷. Besides natural background resistomes, soil also receives repeated inputs of manure, slurry, biosolids, irrigation water, and agrochemicals, and is therefore a logical place to ask whether land use affects resistance profiles. In a study of soils from eleven provinces in China spanning agricultural soils

including tea plantations and forest land, Wu and colleagues found that agricultural soils had the highest abundance and diversity of ARGs, followed by tea plantation and forest soils¹⁸. The study also identified strong associations between ARG profiles, mobile genetic elements, and microbial community structure, supporting the idea that land use helps shape the ecological context within which resistance determinants persist and circulate. Agricultural soils should therefore be understood not only as reservoirs of resistance, but also as hubs within wider AMR circulation pathways. Runoff, erosion, artificial drainage, and leaching can export resistant bacteria, ARGs, pathogens, nutrients, and co-selective contaminants from amended or intensively managed soils into rivers, sediments, and groundwater^{19–21}. At the same time, reuse pathways, including irrigation with reclaimed water, manure and slurry application, and biosolids redistribution, can return urban, livestock, and wastewater-associated microbial and chemical burdens to land. These reciprocal flows connect soils to freshwater systems, crops, food chains and downstream human and animal exposure, making soil management central to both AMR persistence and landscape-scale dissemination.

These findings show that soils are not homogeneous AMR sinks, and that soil pH, structure, particle size, water content, temperature, nutrients, land-use type, management intensity and landscape connectivity are important. Furthermore, they indicate that the effect of land use is not reducible to the simple presence or absence of antibiotic residues. Soil pH, nutrients, metals, microbial composition, and management history all interact. This is relevant for soil health and soil microbiomes. A review on land-system change and AMR should therefore treat soil function and resistome structure together. Nutrient enrichment shifts in carbon availability, disturbance of microbial competition and repeated manure additions can plausibly alter both ecosystems functioning and the probability of pathogen persistence or horizontal gene transfer^{22–24}. AMR processes are also likely to be spatially heterogeneous within agricultural landscapes^{19,25}. Fields, margins, riparian zones, wetlands, drainage ditches, and manure application areas can differ markedly in hydrology, microbial communities, organic matter inputs, and chemical exposure. Selection and mobilisation of resistance are therefore unlikely to occur uniformly across land-use classes, but may be concentrated in hotspots where resistant organisms, ARGs, mobile genetic elements, nutrients and co-selective chemicals overlap.

It is also imperative to consider whether manure enriches pathogenic bacteria, including subclinical burdens relevant to host susceptibility. A substantial proportion of the agricultural AMR literature has focused on the occurrence, diversity and abundance of ARGs in manure-amended soils and other agricultural environments^{26,27}, with comparatively less attention given to how land management influences the abundance, fitness or virulence of opportunistic pathogens in soil and near-soil habitats. Therefore, bringing together resistome studies, pathogen ecology and immunology would strengthen the review and sharpen future research priorities.

Climate-driven land-use transitions and adaptation pathways

One distinctive pathway is that climate stress can alter land-use decisions and production systems in ways that may either increase or redistribute AMR risks. These transitions are highly context dependent and should not be interpreted as a universal shift from crops to livestock or as necessarily leading to higher antimicrobial use. Climate change is experienced by farmers through crop failure, yield instability, unreliable water supplies, altered pest and disease pressure, flooding, drought, labour constraints, and market risk^{28,29}. In some settings, these pressures may encourage greater reliance on livestock, poultry, dairy or aquaculture while in others, farmers may intensify irrigation, use treated or untreated wastewater to maintain crop productivity, change crop types, diversify into mixed farming systems, or alter manure and organic waste management. Each pathway creates different combinations of microbial, chemical and exposure risks relevant to AMR. Such transitions may create new AMR-relevant exposures, but their effects on the selection, persistence and dissemination of AMR, and on opportunities for human and animal exposure, depend on production intensity, animal health and welfare, antimicrobial stewardship, water

source, waste treatment, manure management, and regulatory context. Taking a more integrated planetary health framing extends the analysis beyond farming and veterinary sectors, building on One Health while allowing climate, land-use, livelihood, and environmental pathways to be explored in greater depth.

Recent evidence also suggests that drought can directly reshape soil resistomes³⁰. Shan and colleagues found that drought enriched both antibiotic biosynthesis genes and antibiotic resistance genes across multiple soil metagenomic datasets, and their soil microcosm experiments suggested that drying concentrates natural antibiotics in soil pore water, intensifying selection for resistant bacteria. This adds an important mechanism to the climate–land–AMR pathway where climate stress may increase AMR risk not only by shifting production systems towards livestock or aquaculture, but also by changing the selective environment within soils themselves. Commentary and field-based work from India have argued that climate stress can increase poultry dependence and create conditions in which disease pressure, limited husbandry knowledge and antibiotic use become intertwined³¹. Related work from Karnataka in India linked livestock disease outbreaks to climatic variables, including precipitation and vapour pressure, and highlighted implications for livelihoods and antimicrobial use³². These studies are not globally representative, but they illustrate a mechanism of broad significance whereby climate stress can alter production decisions in ways that may increase or intensify antimicrobial use. That mechanism may also be relevant beyond poultry, for example in dairy or inland aquaculture systems.

The scientific value of this argument lies in its pathway logic because climate change affects the viability of crops, which changes land use and farmer decision-making, which further changes animal density and health risk, subsequently increasing antimicrobial use and waste generation, which in turn alters soil and water exposure. Few AMR reviews connect these steps explicitly, but it is important to acknowledge that not all transitions are the same. Some shifts may increase risk mainly through animal crowding and veterinary drug use while others may act through feed production displacement, wastewater generation or manure management.

Intensive livestock production, waste, and manure pathways

A parallel set of literature, less dependent on climate case studies, has examined the way industrial or concentrated livestock production systems can shape AMR risk. Stevenson's review of industrial livestock production³³ emphasised how high stocking densities, animal crowding, disease transmission, poor welfare, and intensive production inputs can reinforce one another. High animal densities can facilitate pathogen transmission, while physiological stress and suboptimal welfare may increase susceptibility to infection. Furthermore, this can increase the frequency of therapeutic, prophylactic or metaphylactic antimicrobial use, which in turn strengthens selection pressure for resistant organisms. These interacting pressures can therefore, create a self-reinforcing cycle of disease burden, antimicrobial dependence, and AMR selection alongside broader zoonotic and environmental risks³³.

For land-systems, the most critical point is that livestock intensification restructures landscapes of waste. Geographically concentrated animal production can restructure landscapes of waste by accumulating manure, slurry, pharmaceutical residues, resistant bacteria, and nutrients in relatively small areas³⁴. Many intensive systems also depend on imported feed³⁵, which displaces part of the land-use footprint elsewhere while concentrating waste and AMR-related pressures locally.

This matters because manure does not simply return nutrients to land. It can introduce antimicrobial residues, heavy metals, resistant bacteria, ARGs and pathogens into soils, and then into drainage networks, sediments, crops, and water supplies. Manure is therefore both a fertility resource and a potential AMR vector across terrestrial, aquatic and aerial pathways. Livestock housing, manure handling and land application can also generate bioaerosols containing resistant bacteria and ARGs, creating opportunities for local and downwind dispersal^{36–38}. Aerial transport may therefore connect intensive livestock systems with surrounding agricultural land, surface

waters, neighbouring communities and other animal populations^{38,39}, although the viability, exposure dose and health significance of detected airborne resistance determinants remain important areas of uncertainty³⁹. This duality is scientifically and politically important because it shifts the question away from whether manure should be used, and towards the conditions under which organic waste recycling can support soil fertility while minimising antimicrobial residues, resistant organisms, ARGs and co-selective pressures. This is particularly relevant under climate and land-system change, where elevated CO₂, altered fertiliser regimes and organic fertiliser substitution can modify both crop yield and soil ARG profiles, as demonstrated in rice systems⁴⁰. In parallel, manure application method, timing, incorporation, rainfall timing, and soil conditions influence the fate and transport of veterinary medicines after land application. The next step is to connect these chemical fate pathways to soil microbiome responses, ARG persistence and mobilisation, pathogen ecology and ultimately AMR risk.

Animal health under climate stress in semi-extensive systems is also an important issue to consider. Even where production is not fully industrialised, higher incidence of conditions such as mastitis may increase reliance on antimicrobials. This highlights that AMR risk is not confined to one production model, rather emerges from interactions between climate stress, animal health and welfare, husbandry, veterinary access, economics, and waste handling. Therefore, we consciously avoid presenting intensive and extensive systems as simple opposites. Instead, we highlight the need to elucidate which combinations of animal density, animal welfare stressors, environmental pressures, disease burden, antimicrobial use, stewardship, and waste management most strongly drive AMR.

Aquaculture as a land- and water-system interface

Aquaculture sits awkwardly in many AMR frameworks because it is neither straightforwardly terrestrial nor fully separable from land use. It may be recognised both for its importance and the difficulty of obtaining robust antimicrobial use data. Aquaculture often sits at the intersection of aquatic animal health, food production, freshwater management, environmental protection and antimicrobial stewardship⁴¹, creating governance challenges when these policy domains are regulated or monitored separately.

We acknowledge that aquaculture is a rapidly growing food production sector with documented interactions with surrounding ecosystems, including water abstraction, effluent release, organic waste and nutrient loading, disease transmission, antimicrobial exposure⁴² and irrigation with reused wastewater. In some landscapes, aquaculture ponds are located near rice paddy fields or other irrigated crops, allowing pond water or effluent to be reused for irrigation. Such linkages can recycle nutrients and organic matter, but may also redistribute resistant bacteria, ARGs, antimicrobial residues and co-selective contaminants across the aquatic–terrestrial interface. Some of the same drivers identified in terrestrial farming also operate in aquaculture, especially at high stocking densities, disease events, prophylactic and metaphylactic treatment, and waste discharge. Furthermore, aquaculture may become more attractive where climate stress, rising protein demand or market pressures undermine crop production, making it part of a broader land-system adaptation story rather than a separate sector.

At the same time, the evidence base remains geographically uneven. International studies provide important evidence for the mechanisms linking aquaculture, antimicrobial use and environmental AMR dissemination, their direct transferability to the UK may be limited by differences in farmed species, production intensity, antimicrobial-use practices, hydrology, effluent management and regulatory frameworks. Therefore, aquaculture is an area in which surveillance, antimicrobial-use data, environmental monitoring, data transparency, and case-study development are still needed. These aquatic–terrestrial linkages make aquaculture an important interface for AMR circulation, particularly where pond water, effluent, sediments, or organic wastes are exchanged with surrounding agricultural land, irrigation networks, or receiving waters. The priority is therefore to better characterise antimicrobial use, effluent quality, microbial and chemical exposures, and the extent to which aquaculture-derived flows contribute to downstream AMR selection and dissemination.

Urban expansion, informal settlements, and wastewater landscapes

Rapid urbanisation and informal settlements remain comparatively underrepresented in environmental AMR frameworks^{43,44}. Urban land-system change is not just a matter of more people living in cities. It involves conversion of peri-urban farmland, increased impervious surfaces, storm-water concentration, inadequate sanitation, intensified waste generation and new spatial juxtapositions between people, animals, industry, and waterways, all of which are relevant to AMR.

Nadimpalli and colleagues highlight the risk of environmental AMR transmission in these settings because of the high density of humans, livestock and vermin living in close contact under conditions of limited sanitation, contaminated drainage and elevated exposure⁴³. For example, Mphasa et al. have shown elevated levels of resistant pathogens in urban waste piles in Blantyre, Malawi⁴⁵ and Omulu et al. identified environmental and sanitation variables as predictive for the abundance of antibiotic-resistant *E. coli* in informal households in Nairobi, Kenya⁴⁶. These data highlight informal urban settlements as areas of structurally produced risk, which has been argued as an environmental injustice⁴⁷. This is not a minor or temporary issue since more than one billion people already live in informal settlements globally, and this number could rise dramatically by 2050⁴⁸. Within the context of land-system change and AMR, rapid urbanisation should not be presented as background context but as a central pathway through which AMR risks may intensify.

Wastewater systems are central to this argument since they collect organisms, genes, antibiotics and chemicals from hospitals, households, agriculture, industry, and runoff, creating environments in which microbial interaction and gene exchange are likely⁴⁹. Even where treatment reduces biomass, ARGs, resistant bacteria, pharmaceuticals and microplastics may remain in effluent or sludge. Through organic waste management processes, biosolids applied to agricultural soils can reintroduce urban-origin contaminants into rural environments^{50,51}. Wastewater environments provide ideal conditions for protist–bacteria interactions due to high microbial density, nutrient availability and exposure to complex mixtures of antibiotics, pesticides, biocides and metals¹². This is the kind of circularity that a land-system perspective can reveal. It shows that urban and rural AMR are not separate domains but linked phases in the same landscape metabolism.

Other key areas that need further review in urbanising catchments include altered hydrology, stormwater runoff, sewer overflows, household and industrial biocides, surfactants, disinfectants and wildlife-mediated dispersal, all of which can influence how microbial and chemical contaminants are mobilised through urban drainage networks and receiving waters. These points can be brought together effectively by treating cities as chemical as well as microbial landscapes. Urban surfaces alter runoff velocity and direction while household and industrial chemicals create co-selection pressures. Subsequently, open waste or water bodies attract birds and other wildlife that may move resistant organisms across long distances. Airborne dissemination provides an additional connection between urban infrastructure and surrounding environments. Wastewater treatment processes, particularly aeration and sludge handling, can generate bioaerosols containing resistant bacteria and ARGs^{52–54}, while composting facilities, waste handling, traffic-associated particulate matter and resuspended urban dust may provide additional sources^{54,55}. These materials can be transported downwind or deposited onto land and water, creating air–land and air–water pathways that are rarely incorporated into catchment-scale AMR assessments. Urban form may further modify these processes through differences in vegetation cover, surface roughness, particulate matter, temperature and airflow. Recent work^{53,54}, has for example, identified associations between green space, urban settings, seasonality and airborne ARG profiles⁵⁶. Consequently, urban AMR surveillance could also account for air alongside wastewater, surface water and soil where aerial dispersal is a plausible connection between sources and exposed populations.

Conflict-affected and environmentally disrupted settings

Conflict-affected and environmentally disrupted settings represent acute forms of land-system breakdown. We define conflict as that which is not only violent, but broader forms of environmental conflict and disruption, within the land-system framing. Conflict can rapidly alter land cover, waste handling, sanitation, healthcare access, veterinary services, displacement patterns, livestock movement, and environmental contamination^{57–59}. It may therefore create conditions similar to or overlapping with informal settlements, but with additional features such as healthcare collapse, mixed population movements, and damaged infrastructure.

The current evidence base is still comparatively fragmented. However, conflict-affected settings, like urban informal settlements, can reasonably be described as intensified environments of exposure, crowding and system breakdown that are relevant to AMR. They also reveal the profound importance of infrastructure and governance in shaping environmental transmission. We believe that conflict acts as a cross-cutting amplifier of urban and rural AMR risk, socioeconomic drivers, and environmental hazard formation.

Deforestation, habitat fragmentation, and zoonotic interfaces

Agricultural expansion, road building and land conversion increase contact between wildlife, livestock and people⁶⁰. Although zoonotic pathogen transmission is not the same as AMR transmission, the same landscape changes that increase spillover risk can also modify antimicrobial use patterns, waste exposure, and opportunities for microbial exchange. Habitat fragmentation may also alter wildlife movement and resource use, increasing contact with farms, landfills, and waterways.

The link to AMR is therefore indirect but real where future analyses should carefully review how deforestation and habitat fragmentation as processes may increase interface intensity rather than as deterministic causes of resistance. Where land conversion expands livestock systems into previously less disturbed areas, antimicrobial use and waste exposure may also rise. Where wildlife increasingly exploits human-associated resources, including pasture, crops, livestock feed, food waste, landfill material, sewage-impacted waters and aquaculture waste, opportunities for AMR dispersal may increase. Additionally, work is needed to understand and highlight AMR as the bridge between zoonotic risk, biodiversity change, and wildlife-mediated dissemination.

Biodiversity loss, soil function, and microbial resilience

Biodiversity loss is often discussed in relation to macrofauna and flora, but for AMR the microbial dimension is critical. Microbial diversity supports nutrient cycling, soil structure, decomposition, and competitive interactions that can suppress some pathogens or alter the persistence of resistance determinants. Importantly, highly diverse resident soil microbial communities can also provide a biological barrier to the establishment and persistence of introduced microorganisms. Experimental work has demonstrated an inverse relationship between soil microbial diversity and survival of an introduced *Escherichia coli* O157:H7 strain, with more diverse communities restricting invader persistence through more complete resource use and stronger competition⁶¹. This ‘invasion resistance’ suggests that disturbance or loss of microbial diversity could weaken colonisation barriers and increase opportunities for introduced resistant organisms to persist and disseminate, although the extent to which this translates specifically into AMR transmission requires further investigation^{61,62}. Disturbance, pollution, and repeated organic waste application may influence diversity or reorganise microbial communities in ways that favour resistant taxa potentially increasing horizontal transfer of resistance genes via mobile genetic elements. In this sense, biodiversity loss and AMR are not parallel crises, rather they may be mechanistically linked through changes in ecological resilience. Protist–bacteria interactions can influence both the composition and function of microbiomes by preferentially removing susceptible cells while enriching for phenotypes associated with survival under predation pressure, including biofilm formation, intracellular persistence, stress tolerance and, in some cases, antimicrobial resistance traits¹². In

addition to their role as predators, many protists act as intracellular hosts that provide protected niches for bacteria¹¹, facilitating persistence under adverse environmental conditions and potentially enhancing horizontal gene transfer within confined cellular environments. These processes position protists not only as regulators of microbial diversity but also as potential amplifiers of resistance dynamics, particularly in soils, sediments, and aquatic systems where they are abundant. Incorporating protist-mediated trophic interactions into studies of soil function and microbial resilience would therefore provide a more mechanistic understanding of how land-use change and environmental disturbance reshape the ecological conditions that govern the selection, maintenance, and dissemination of antimicrobial resistance.

Soil microbiomes are central to understanding how land management influences the balance between ecosystem function and resistome accumulation. Rather than measuring only ARG abundance, future studies could ask how land-use intensity changes microbial interaction networks, pathogen suppression, nutrient cycling, and host exposure at the same time moving the field closer to a true ecological epidemiology of AMR.

Novel entities, co-selection and antifungal resistance

One of the most scientifically and policy-relevant opportunities for this paper is to strengthen treatment of co-selection and antifungal resistance. Azole-resistant *Aspergillus fumigatus* has become one of the clearest examples of an AMR problem that cannot be understood without environmental selection. Environmental fungicide use, particularly in horticulture and agriculture, has long been implicated in selecting resistance traits that reduce the effectiveness of clinically important azoles^{63–67}. Recent work has reinforced the concern, including evidence of pan-azole and multi-fungicide-resistant *A. fumigatus* in the United States⁶⁸, UK evidence that plant-associated *Fusarium* species including *Fusarium temperatum* occur in forage maize systems⁶⁹, and coordinated warnings from European agencies about preventing environmental resistance selection⁶³. The relevance to land-system change is straightforward where climatic conditions, crop disease pressures and land-management choices can all influence fungicide reliance, while compost, plant waste and agricultural residues can provide the substrates in which environmental *Aspergillus* populations are exposed.

The broader concept here is co-selection where antibiotics are not the only relevant selective agents. Metals, disinfectants, surfactants, microplastics and other contaminants may contribute to the persistence, selection or spread of resistance determinants, although the strength and direction of these effects are compound-specific and context-dependent. For example, while some non-antibiotic chemicals can impose selective or co-selective pressures, recent evidence also shows that certain non-antibiotic pharmaceuticals can be toxic to bacteria without necessarily driving cross-resistance to antibiotics⁷⁰. This highlights the need to distinguish between chemical toxicity, selection for tolerance and selection for clinically relevant antimicrobial resistance, rather than assuming that all chemical stressors promote AMR. We therefore note that chemical policy and AMR policy are intricately connected, but that their integration should be guided by compound-specific evidence. This is especially important in the UK context, where the 2024–2029 AMR National Action Plan explicitly includes the environment, agriculture, and the need for action across sectors⁷¹.

Novel entities and industrial chemical pollution

Land-system change also includes the conversion of agricultural, peri-urban, or riparian land into industrial zones, waste-processing areas and mixed-use urban-industrial landscapes. These settings can generate complex pollution mixtures, including heavy metals, solvents, dyes, detergents, biocides, pharmaceutical residues and untreated or partially treated wastewater. When industrial effluent enters the same waterways as agricultural runoff, hospital wastewater and domestic sewage, these rivers and drains become chemically and microbiologically mixed environments in which antimicrobial resistance may be selected, maintained and disseminated.

This issue is particularly important in rapidly industrialising and urbanising regions, where waste infrastructure, environmental regulation

and occupational protections may not keep pace with economic growth. Doron's work on waste, structural violence and AMR in India is useful here because it reframes waste not only as a pollution problem, but also as a question of labour, inequality, infrastructure and uneven exposure⁷². In this framing, the environmental persistence and dissemination of antimicrobial-resistant organisms and resistance determinants, together with opportunities for human exposure, are shaped by the co-location of contaminated environments, precarious waste work, inadequate sanitation, and limited access to healthcare, rather than through individual behaviour alone.

There is substantial global evidence that heavy metals and other co-selective contaminants can contribute to the maintenance and enrichment of AMR in environmental microbial communities. Studies across aquatic, terrestrial and wastewater-impacted environments have demonstrated associations between metal pollution, metal-resistance genes, antibiotic-resistance genes, integrons and bacterial community composition. For example, comparative work in Indian and UK rivers has shown elevated resistance profiles at sites affected by metal and industrial pollution⁷³. This supports the argument that novel entities and industrial contaminants should be treated as AMR-relevant selective pressures, especially where they coincide with sewage, hospital wastewater, agricultural runoff, and high human exposure.

Wildlife vectors and landscape connectivity

Another key area for consideration is that gulls feeding on landfills and roosting in waterways should be thought of as a pathway connecting polluted urban environments to remote settings. Reviews have identified wildlife, especially gulls, as neglected components of AMR epidemiology in anthropogenic landscapes. Empirical work provides evidence that gulls can acquire resistant bacteria from human-associated sources and then disperse them across regions and even between continents⁷⁴.

Movement-based and field studies show that wildlife can connect multiple AMR-relevant environments⁷⁵, including farms, wastewater systems, landfills, freshwater bodies, and coastal waters. Black-headed gulls have been shown to use wastewater treatment plants and connect different anthropogenic sites while carrying resistant organisms⁷⁶. However, similar wildlife–farm–water interactions are likely to involve a wider range of species. In the UK, wildfowl such as geese are widespread across agricultural catchments and waterbodies and have been identified as relevant targets for AMR and pathogen surveillance because they move between pasture, livestock areas, reservoirs, and surface waters⁷⁷. Coastal mammals may also act as sentinels of human-associated environmental contamination. Recent work⁷⁸ on seals from Scottish and Liverpool Bay coastal waters detected variation in ARGs, mobile genetic elements and integrons in seal faeces, including differences between populations near and far from large human populations. Collectively, these examples show that wildlife should be considered as part of landscape connectivity, rather than as isolated reservoirs of resistance.

This literature demonstrates that wildlife is part of the land-system AMR story not because wildlife is the origin of the problem, but because wildlife exploits the ecological opportunities created by human waste systems. It also reinforces the argument that landscape connectivity is central. Landfills, wastewater plants, agricultural fields, and surface waters should not be treated as independent systems when mobile scavengers and waterbirds regularly move among them. We therefore posit that wildlife-mediated dispersal is added within the pathway framework, while making clear that the dominant drivers remain anthropogenic waste, land use, and chemical exposure.

Nature-based solutions and land-system interventions

Land-system change can also create opportunities for intervention, and examples of effective landscape design are as important as catalogues of risk. For example, constructed wetlands are one of the clearest examples. A growing literature shows that well-designed wetlands can reduce contaminant loads, including antimicrobials, resistant bacteria and ARGs, while also providing co-benefits for habitat, carbon storage, and water quality⁷⁹.

Table 1 | Illustrative datasets for land-use and urban change

Database	Maintained by	Link	Used in (example)
Normalised Difference Vegetation Index (NDVI)	NASA	earthdata.nasa.gov/topics/land-surface/normalised-difference-vegetation-index-ndvi	Assessing vegetation density and health in relation to soil resistomes.
Vegetationmap4Africa	University of Copenhagen	vegetationmap4africa.org	Mapping ecological gradients in sub-Saharan agricultural zones.
Tianditu (MapWorld)	Chinese Government	tianditu.gov.cn	Correlating ARG prevalence with diverse land-use types.
ISGlobal City Index: Green space	ISGlobal	isglobalranking.org/ranking/#green	Studying the impact of urban greening on environmental AMR.
Urban Expansion Data	MIT	cityform.mit.edu/projects/measuring-urban-expansion	Tracking the footprint of urbanisation on catchment hydrology.
Urban Expansion Prediction Models	ISPRS	isprs-archives.copernicus.org/articles/XLVIII-4-W17-2025/227/2026/	Modelling future hotspots of environmental transmission.

Methodological resource for pairing environmental AMR sampling with established land-use and expansion metrics.

Recent work in chalk-stream catchments has explored their role as barriers between wastewater treatment outputs and sensitive receiving waters⁷⁹. These systems are not universal fixes, but they provide a good example of how landscape design can be used to interrupt AMR-relevant pathways rather than merely monitor them. Related work⁸⁰ on natural filtering of *E. coli* suggests that vegetation, sediments, biofilms, and microbial food-web interactions can contribute to the attenuation of faecal indicator bacteria, although performance will depend on hydrology, loading rates, season, and system design.

Nature-based and integrated treatment approaches may also be relevant at aquaculture–agriculture interfaces. Constructed wetlands, algal treatment systems, sedimentation ponds, and integrated aquaculture designs could reduce nutrient loading, organic waste, antimicrobial residues, and microbial contaminants before effluent reaches receiving waters or is reused for irrigation⁸¹. However, these approaches should be evaluated as managed intervention points rather than assumed to be inherently protective, with monitoring of ARGs, viable resistant organisms, antimicrobial residues, and co-selective contaminants.

Furthermore, mangrove restoration and integrated aquaculture landscapes have also been proposed as ways to reduce effluent impacts⁸², improve ecosystem resilience and potentially lower some forms of antimicrobial use. The literature here is more heterogeneous, and some mangrove systems are themselves contaminated by antimicrobials and ARGs, particularly where aquaculture and urban pressures are high. Nature-based solutions work when they are appropriately designed, governed, and monitored, not simply because they are green.

Available data, surveillance, and land-use datasets

A critical priority is the practical integration of diverse evidence sources, ranging from remotely sensed vegetation cover and urban expansion products to historical soil archives. We argue that one of the most immediate opportunities for advancing the field is the combination of high-resolution land-use data with environmental AMR sampling. Currently, many studies relegate land use to coarse metadata or static categories. However, there is substantial scope to link resistance measurements to dynamic variables such as vegetation indices, urban expansion trajectories, drainage characteristics, and historical management practices.

The datasets summarised here (Table 1) are not only an informational resource but also act as a methodological roadmap for spatially explicit, land-use-aware surveillance. This agenda requires leveraging strategic partnerships and institutional assets, such as the VMD/RUMA livestock usage datasets and long-term soil libraries, most notably the 167-year-old archive at Rothamsted Research in the UK, which allows for the longitudinal tracking of AMR in relation to animal manure application.

A scientifically mature review must, however, acknowledge existing structural constraints. Livestock antimicrobial usage data remains

commercially sensitive, aquaculture data is often proprietary or sparse, and environmental surveillance is currently fragmented across disparate media such as soil, air, and wildlife. Rather than viewing these gaps as a rationale for caution, they should be utilised as a diagnostic map for identifying where future surveillance infrastructure is most urgently required.

Global framing and UK-focused implementation

While the most illustrative case studies of climate-driven land-system transitions often emerge from the Global South, including rapidly urbanising Asian settings or climate-stressed agricultural zones in India and sub-Saharan Africa, the underlying mechanisms are generalisable across land systems. Input intensification, habitat reorganisation, and enhanced connectivity also operate in Global North contexts such as the UK, although through different combinations of agricultural intensification, wastewater and biosolids management, urban expansion, catchment modification, and climate adaptation planning.

This makes the UK an important implementation context rather than an exception to the global evidence base. The UK 2024–2029 AMR National Action Plan (NAP) explicitly adopts a transdisciplinary “One Health” framing that encompasses human health, agriculture, and the environment⁷¹. A planetary health framing can extend this further by linking AMR policy to land-use planning, water management, waste regulation, chemical governance, biodiversity protection, and climate adaptation.

The UK also has significant capacity for leadership in this domain through its established infrastructure for wastewater regulation, environmental monitoring, and research–policy translation via agencies such as SEPA and the Environment Agency. Land-system AMR research should therefore operate at two levels, such as synthesising global ecological mechanisms that explain why land-system change matters and using national contexts such as the UK to identify tractable priorities for surveillance, intervention and governance.

From environmental pathways to practical intervention

Several research priorities emerge from this review. They aim to move the field from compartmentalised surveys towards integrated landscape epidemiology, while also identifying practical intervention points where AMR selection, mobilisation and transmission can be reduced.

1. *Pathway-based surveillance*: Future study designs should move beyond measuring resistance genes in single compartments, such as soil or water, towards tracing the movement of resistance determinants across connected waste–soil–water–air–crop–wildlife–animal–human pathways. These pathways include manure and slurry application, biosolids recycling, wastewater irrigation, drainage, runoff, aerosolisation and atmospheric deposition, groundwater and surface-water transport, crop contamination, and wildlife movement. A particular priority is to

resolve the directionality, reciprocity, and relative importance of these pathways under different land-use, hydrological and governance contexts.

2. **Spatial land-use integration:** Remotely sensed land-use and vegetation datasets should be routinely integrated into AMR studies at spatial and temporal scales that reflect hydrological connectivity, ecological linkages, and land-use change over time.
3. **Antifungal resistance (AFR) and cross-kingdom ecology:** AFR must be fully incorporated into environmental AMR frameworks, particularly at the intersection of crop protection policy, clinical treatment efficacy, and climate-driven fungal disease pressures. Future work should also consider how interactions among fungi, bacteria, protists, viruses and other micro-eukaryotes shape resistance dynamics through predation, biofilms, host-associated persistence, horizontal gene transfer, pathogen suppression, and co-selection. CLIMAR is working closely with the Fungal One Health and Antimicrobial Network, another BBSRC-funded network, to further explore the intersections of antifungal and antibiotic resistance within this broader ecological context.
4. **Urbanisation and informal settlements:** Rapid urbanisation must be elevated from background context to a central pillar of the environmental AMR agenda.
5. **Longitudinal and comparative designs:** There is an urgent need for long-term studies capable of distinguishing the specific effects of land-use intensity from background environmental contamination.
6. **Practical intervention points:** Future work should identify where AMR transmission can be reduced across connected landscapes, including manure and slurry management, wastewater and biosolids treatment, runoff control, livestock housing and welfare, landfill management, antimicrobial stewardship, and nature-based treatment zones. Interventions should be evaluated for their ability to reduce ARGs, viable resistant organisms, pathogens, co-selective chemicals, and exposure risks.

Methodologically, these priorities require transdisciplinary approaches that combine culture-based microbiology, metagenomics, high-throughput qPCR, chemical monitoring, standardised sampling, metadata collection and spatial modelling with landscape ecology, remote sensing, and participatory community-led approaches grounded in people's lived realities. Institutionally, this will require stronger interfaces between environmental regulators, agricultural specialists, land-use scientists, public health agencies, and communities affected by environmental AMR risks, including those in displaced, informal or infrastructure-limited settings.

Conclusion

Land-system change is not a peripheral cofactor in AMR; it is a structuring process that influences where resistance is selected, how it is maintained and the routes through which it is disseminated. Agricultural intensification, urban expansion, informal settlement growth, and aquaculture development alter the ecological and chemical conditions under which micro-organisms, antimicrobial residues, co-selective contaminants, animals, waste streams, and people interact. Climate change further modifies these relationships by affecting crop viability, livestock production, hydrological connectivity, drought and flood dynamics, and the movement of waste and water across landscapes.

The distinctive contribution of this review is to reposition land-system change from a background contextual factor to an organising determinant of environmental AMR. Existing One Health and environmental AMR frameworks have established the importance of environmental selection, reservoirs and transmission pathways^{4–6}. Our synthesis extends this perspective by asking how those processes are structured spatially through land use and landscape change. By framing agricultural, urban, aquatic and waste-associated processes through altered input intensity, habitat reorganisation and enhanced connectivity, we provide a landscape-scale structure for linking the selection, persistence and dissemination of resistance with climate adaptation, infrastructure, biodiversity and governance. This

perspective also identifies practical opportunities to integrate spatial land-use information with AMR surveillance and to target landscape intervention points where the mobilisation and transmission of resistance may be reduced. For CLIMAR and the wider AMR research community, the priority now is to translate this pathway-based understanding into testable evidence and practical intervention points. This requires moving beyond compartment-specific surveillance towards integrated assessment of connected soils, waters, livestock systems, wildlife, wastewater infrastructure, and human exposure. The available evidence is sufficient to justify treating land-system change as a core determinant of environmental AMR risk, while also highlighting where longitudinal datasets, mechanistic studies and policy-relevant surveillance are most urgently needed. Addressing AMR at this scale will require coordinated action across microbial ecology, land-use planning, agriculture, water management, climate adaptation, and public health.

Data availability

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Additional information

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