

European profiling of urban anthrosols to assess assembly dynamics, ecological resilience, and microbiological hazards along climatic gradient.

Dynamiques d'assemblage, résilience écologique et risques pathogènes des anthrosols urbains le long des gradients climatiques en Europe.

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RÉSUMÉ

L'urbanisation transforme les écosystèmes et menace la santé humaine, animale et environnementale notamment par l'accumulation de polluants et de résidus issus des activités anthropiques. Parmi les compartiments urbains qui en découlent, les anthrosols urbains (AU) restent particulièrement sous-étudiés alors qu'ils peuvent fortement influencer d'autres compartiments hydriques de la ville. Ces matrices pédogéniques émergentes se développent sur les surfaces imperméables par l'accumulation et la transformation microbienne de résidus technogéniques et organiques. Nos premiers résultats à Lyon (France) montrent que les AU constituent des réservoirs de polluants et de contaminants microbiologiques, incluant des bactéries fécales et des pathogènes. Les hydrocarbures aromatiques polycycliques (HAP) structurent fortement le microbiome des UA en renforçant la cohésion fongo-bactérienne et sélectionnant des interactions entre dégradeurs d'hydrocarbures et pathogènes. Cependant, il manque encore un cadre conceptuel formel et une compréhension écologique à grande échelle de ces UA. Nous présentons une initiative paneuropéenne couvrant des villes de plusieurs zones bioclimatiques, et fondée sur approche intégrative incluant analyses multi-polluants, métabarcodages d'ADN multi-domaines et quantification des pathogènes. Des microcosmes expérimentaux permettront d'évaluer la résilience des pathogènes et la mémoire écologique des UA sous différents scénarios d'îlot de chaleur urbain. Cette initiative vise à établir une base de données européenne des UA, un cadre opérationnel et des outils prédictifs des risques sanitaires afin d'identifier des zones urbaines prioritaires de gestion, tout en invitant villes et équipes de recherche à collaborer dans le cadre de ce projet dédié à la santé environnementale urbaine.

ABSTRACT

Urbanization reshapes ecosystems and threatens human, animal, and environmental health notably through the accumulation of pollutants and wastes derived from anthropogenic activities. Among the resulting urban compartments, urban anthrosols (UA) remain particularly understudied, even though they can strongly influence other hydric compartments. Our results from Lyon (France) show that UA act as reservoirs of hazardous substances and microbial contaminants, including fecal bacteria and pathogens. Polycyclic aromatic hydrocarbons (PAHs) strongly structured the UA microbiome, reinforcing fungal–bacterial cohesion and selecting cross-domain interactions of hydrocarbon degraders and pathogens that serve as indicators of environmental health hazards. Yet, a formal conceptual framework and large-scale ecological understanding of UA are still lacking. We present a Pan-European initiative targeting cities across different bioclimatic zones to characterize UA through integrative pollutant profiling, multi-domain eDNA metabarcoding, and pathogen quantification. Experimental microcosms will assess pathogen resilience and ecological memory under UHI scenarios. This initiative aims to build a European UA database, an operational framework, and predictive microbiological risk-assessment tools to identify priority urban areas requiring tailored management, while inviting cities and research teams to collaborate in this project dedicated to urban environmental health.

MOTS CLÉS

Anthrosols ; Microbial biogeography ; One Health ; Urban health hazards ; Urban microbiome

1 INTRODUCTION

1.1 Urban anthrosols as an emerging city compartment

Urbanization is accelerating globally, with over 65% of the population expected to live in cities by 2050, intensifying human, animal, and environmental health risks through the accumulation of persistent contaminants such as PAHs, trace metals (*e.g.*, Cd, Pb, Hg), and urban wastes derived from traffic, industry, and other anthropogenic activities (Lu et al., 2024). Growing evidence indicates that pollutant build-up across urban compartments (air, runoff, deposited sediments) selects for extremophiles and pollutant-tolerant opportunistic pathogens such as *Acinetobacter*, *Mycobacterium*, and *Pseudomonas*, positioning cities as reservoirs for emerging infectious agents (Bernardin-Souibgui et al., 2018; Bouchali et al., 2024).

Among these compartments, urban anthrosols (UA) are emerging, persistent soil-like matrices (**Figure 1**), partially structured by city surface microbial community (also called microbiome), through the sustained accumulation and microbial transformation on impervious urban surfaces of diverse urban-derived wastes, including tire wear particles, brake dust, engine exhaust, runoff-transported like sand, plant debris, spoiled food, fecal matter, and atmospheric pollutants (Lehmann and Stahr, 2007). Unlike weathered technogenic debris (*e.g.* plastics, crushed concrete, food wrappers), UA are mixtures including sub-products of such materials that accumulate on road edges, sidewalks, tree pits, swales, and support synurbic vegetation, scavengers, and microbial decomposers (Niepsch et al., 2025; Dominguez-Lage et al., 2025; Marti et al., 2017).

1.2 Chemical and microbiological risks associated with anthrosols

Urban anthrosols pose dual chemical–biological concerns to human and environmental health, concentrating persistent pollutants such as PAHs and trace metals (*e.g.*, Cu, Zn), alongside pathogenic bacteria including *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and *Bartonella* spp. (Aigle et al., 2021). Both pollutants and microorganisms can disperse across air, soil and aquatic compartments through resuspension, runoff, rainfall-driven wash-off, or wind-driven transport, ultimately contributing to contamination of stormwater networks, rain garden soils, and sediments in retention basins, and thereby increasing human exposure risks (Bernardin-Souibgui et al., 2018). Notably, pathogens such as *Aeromonas caviae* and *Pseudomonas aeruginosa*, often associated with fecal signatures and hydrocarbon degraders, have been detected in stormwater detention basin sediments, urban runoff, and resuspended road deposits, highlighting the potential for cross-compartment microbial transfer and occupational exposure risks (Dominguez-Lage et al., 2025).

1.3 Management challenges and knowledge gaps in urban anthrosol ecology

Municipalities worldwide invest substantial resources in street cleaning to mitigate accumulation of urban residues, which represent a major component of total municipal solid waste (Niepsch et al., 2025). In France alone, ~5 billion tons of street residues are generated annually, incurring economic costs of 300 millions euros. In a mid-size European city like Lyon (1.5 million inhabitants, 530 km²), approximately 25,000 tons are collected each year from more than 2,500 km of roads and public spaces (Grand Lyon, pers. comm.). Although these residues are categorized as urban wastes under the French law (Environmental Code, Articles L541-1 and L541-2) and require specialized treatment (Lipeme Kouyi et al., 2018), street sweeping shows highly variable efficiency, with sediment removal rates as low as ~30% (Amato et al., 2010). Consequently, a substantial fraction of residues persists on urban surfaces, promoting UA formation.

Despite growing awareness of their chemical and microbiological hazards, the ecological status of urban anthrosol microbiomes remains poorly resolved, particularly regarding the mechanisms that drive pathogen enrichment in these pollutant-rich matrices. Fungi likely represent a key yet overlooked structuring component of anthrosol microbiomes: their capacity to degrade PAHs and to facilitate bacterial survival under harsh conditions suggests that fungal–bacterial associations may play a central role in shaping community assembly and enhancing the persistence and spread of opportunistic pathogens in UA.

1.4 Objectives

We aimed at (i) quantify pathogen loads and assess how pathogenic bacteria respond to PAH gradients and fecal contamination inputs; (ii) identify how PAH pollution and abiotic factors jointly structure bacterial and fungal community composition and diversity; and (iii) evaluate the impact of PAHs on fungal–bacterial ecological networks, particularly the emergence of specialized modules enriched in hydrocarbon degraders and pathogenic taxa. By integrating pollutant profiling, qPCR-based pathogen detection, microbial source tracking, and dual-

domain amplicon sequencing, the study aims to unveil the functional biodiversity and ecological state of the urban anthrosols of Lyon.

2 MATERIAL & METHODS

2.1 Sampling strategy

Urban anthrosols (UA) were sampled in three sub-catchments at each of three Lyon urban sites selected for their contrasting socio-urbanistic features (Figure 1): C01, C06, C18 in Chassieu Mi-Plaine (CMP); P04, P05A, P05B in Garibaldi-city center (GRB); and S31, S32, S33 in Vieux Lyon/Montplaisir (VLM), predominantly pedestrian historic districts. Sampling campaigns were conducted in November 2023, April 2024, and June 2024.

2.2 Physico-chemical analysis

Monitored abiotic parameters included total C, N, and P; concentrations of 17 PAHs; major ions (NO_3^- , NH_4^+ , SO_4^{2-} , PO_4^{3-} , Na^+ , K^+ , Mg^{2+}); other elements like aluminium (Al), silicon (Si), phosphorus (P), sulfur (S), chlorine (Cl), titanium (Ti), iron (Fe), manganese (Mn), copper (Cu), zinc (Zn), chromium (Cr), and molybdenum (Mo); and key climatic variables (temperature, radiation and recent rainfall). These variables were jointly analysed by Principal Component Analysis (PCA), providing a comprehensive characterization of urban anthrosol chemistry and pollution patterns across the city of Lyon.

2.3 Microbiome analysis

Genomic DNA was extracted from UA samples for qPCR quantification of microbial markers, including total bacteria, fungi, and key pathogens (*Pseudomonas aeruginosa*, *Aeromonas caviae*, *Staphylococcus aureus*, *Listeria monocytogenes*, *Nocardia* spp.). Quantitative microbial source tracking (qmST) further targeted human (HF183) and dog/fox (Can-Bac) fecal signatures. Bacterial (16S rRNA gene) and fungal (ITS2 of the rRNA operon) amplicons were sequenced to characterize microbial community composition, diversity and structure in UA. Functional inferences were derived from microbial taxonomic profiles to assign potential ecological roles, and identify groups associated with hydrocarbon degradation and infectious outcomes. Microbial community diversity, compositional structure, and bacterial–fungal ecological networks were related to physico-chemical variables, with particular attention to PAH contamination. Correlation analyses were used to quantify the influence of individual and total PAH concentrations on network of microbial partners. Topologies and module structure of networks were investigated. Inferences on taxonomic and functional patterns were performed, and identified synergistic modules involving pathogens driven by PAH selective pressures.

3 RESULTS & DISCUSSIONS

PCA analysis showed that PAH compounds were the primary drivers of the physico-chemical profile of UA, structuring the main environmental gradient and clearly separating urban typologies (Figure 2). PAH concentrations frequently exceeded thresholds for heavily polluted soils ($> 1,000 \mu\text{g}\cdot\text{kg}^{-1}$ total PAHs), revealing heterogeneous but consistently high contamination across Lyon UA.

qPCR assays detected five bacterial groups across Lyon's anthrosols (Figure 2), exhibiting taxa-specific responses to PAH pollution; notably, *Nocardia* spp. ('noc') which showed strong positive correlations with total PAH concentrations.



Figure 1. Sampling sites around Place Guichard subway station (S33, 'VLM' site) in Lyon.

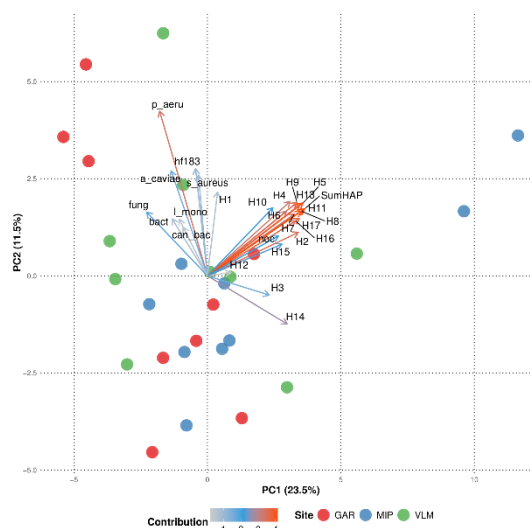


Figure 2. Principal Component Analysis (PCA) of abiotic, HAP, and qPCR variables across urban anthrosol samples.

Only loading vectors for PAHs (H1–H17, SumHAP) and qPCR-derived microbial indicators (bact, fung, p_aeru, a_caviae, s_aureus, l_mono, noc, hf183, can_bac) are shown. Arrow length and direction indicate variable influence on the PCA, and color intensity reflects their contribution to PC1 and PC2.

qMST markers further indicated co-occurrence between fecal inputs and pathogen presence, with *Aeromonas caviae* positively associated with the dog/fox (Can-Bac) fecal marker.

Correlation analyses showed that bacterial and fungal community structures were most strongly shaped by individual and total PAHs, with pyrogenic emissions from incomplete fossil fuel combustion emerging as a key driver for both microbial domains.

Cross-domain network analyses showed that PAH pollution generated more centralized and heterogeneous modules. Notably, the marked decrease in network vulnerability suggests enhanced structural robustness and thus a greater capacity for persistence under pollutant stress in anthrosols. Modules emerging under higher PAH pollution were enriched in positive interactions involving bacterial hydrocarbon degraders and pathogens, and stress-tolerant fungi, highlighting strengthened functional specialization in PAH-polluted anthrosols.

4 CONCLUSION & FUTURE DIRECTIONS

As urbanization intensifies, understanding the ecological behavior and health implications of UA becomes essential within a One Health perspective. Our results showed that UA act as reservoirs of both organic pollutants and microbial hazards, with PAH contamination emerging as a dominant ecological driver that restructures microbial communities and reinforces bacterial-fungal interactions supporting pathogen persistence. Building on these findings, our next objective is to scale up this work to a pan-European assessment of anthrosol functional biodiversity, resilience, and microbiological risk assessment across climatic gradients. This initiative will investigate how physicochemical stressors (PAHs, MTEs, PCBs, PFASs), climate forcing (bioclimatic zones, urban heat island), and ecological connectivity (microbial dispersion, biotic interactions) shape microbial community coalescence in UA. Particular attention will be given to pollutant-microbe co-occurrence, functional convergence in microbial assemblages, and conditions favoring accumulation and growth of pathogens. To achieve this ambitious sampling effort, we are actively seeking partner laboratories across Europe willing to contribute local expertise and support sampling in their respective cities. Collaborations with municipal agencies, environmental observatories, and research infrastructures are also highly welcome. By integrating multi-pollutant profiling, multi-kingdom eDNA, and experimental approaches, the project will seek to develop a predictive framework for anthrosol ecology and to inform sustainable urban management strategies across Europe.

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