

PERSPECTIVE

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The nasal ecosystem as a sentinel interface for One Health surveillance in an era of converging crises

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Abstract

The interconnectedness of human, animal, and environmental health demands surveillance systems capable of predicting cross-boundary threats. We propose a solution already inside us: the nasal microbiome. Positioned at the interface of environmental exposure, zoonotic transmission, and immune regulation, the nasal microbiome could serve as an early-warning system for pandemics, antimicrobial resistance (AMR), and climate-driven health impacts. Emerging evidence supports its predictive capacity, but many applications remain conceptual and require systematic validation. We therefore outline a roadmap for standardising nasal microbiome monitoring across One Health sectors, with the potential to shift global disease surveillance from reactive to proactive and enable timely interventions before threats escalate.

Keywords Nasal microbiome, One health surveillance, Respiratory tract infections, Air pollution and health, Zoonoses, Antimicrobial resistance

1 Introduction

Global health is beset by converging threats: emerging zoonoses, escalating antimicrobial resistance, and climate-amplified diseases. Current surveillance systems, fragmented by sector, reliant on symptom reporting, and slow to connect environmental, animal, and human data, repeatedly fail at the very nexus where these crises collide. When avian influenza A virus H5N1 (H5N1) jumps from poultry to dairy workers or antibiotic-resistant pathogens surge through urban slums, health responses arrive too late. What if we could detect these threats before they manifest as outbreaks?

The nasal cavity, a dynamic crossroads where inhaled environments, zoonotic encounters, and immune defences interact, holds transformative potential. Its microbiome, a living sensor shaped by air, pathogens, and host immunity, offers real-time biological surveillance. Unlike traditional methods, nasal microbial communities shift during sub-clinical stages, signalling risks while interventions might still prevent catastrophe. The One Health approach recognises that the health of humans, animals, and ecosystems are



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interdependent, requiring coordinated action across these domains to prevent and manage emerging health threats.

Consider a Wisconsin dairy farmer: his nasal microbiome, constantly exposed to dust, pathogens, and antibiotics, serves as a living record of the environmental pressures he faces. When influenza viruses disrupt microbial diversity, as shown in avian models where avian influenza A virus H9N2 (H9N2) infection sharply reduces respiratory tract microbiota richness [1], the resulting immune activation mirrors findings in H5N1-infected humans, where excessive cytokine responses drive pathology [2]. Similarly, in Malawian infants, exposure to elevated household particulate matter (2.5 micrometres or smaller) (PM_{2.5}) increased nasopharyngeal carriage of *Streptococcus pneumoniae*, a precursor to childhood pneumonia [3]. During the COVID-19 pandemic, individuals who mount rapid nasal secretory immunoglobulin A (sIgA) responses shed virus for shorter durations, demonstrating how early mucosal immunity can predict infectiousness [4]. These findings compel us to propose nasal microbiome monitoring as an operational pillar of the Quadripartite’s One Health Joint Plan of Action (Fig. 1). Standardised nasal sampling in climate-vulnerable regions and high-risk occupational groups could transform preparedness. Indeed, during the 2022–2023 H5N1 epizootic in Spain, routine polymerase chain reaction screening of asymptomatic poultry workers led to the early detection of two human cases, signals that standard surveillance systems would have likely missed [5].

Nasal microbiome surveillance, therefore, offers a bridge across traditionally disconnected domains. In zoonotic disease monitoring, H5N1 was detected in U.S. dairy workers through the detection of viral ribonucleic acid in nasal and conjunctival samples

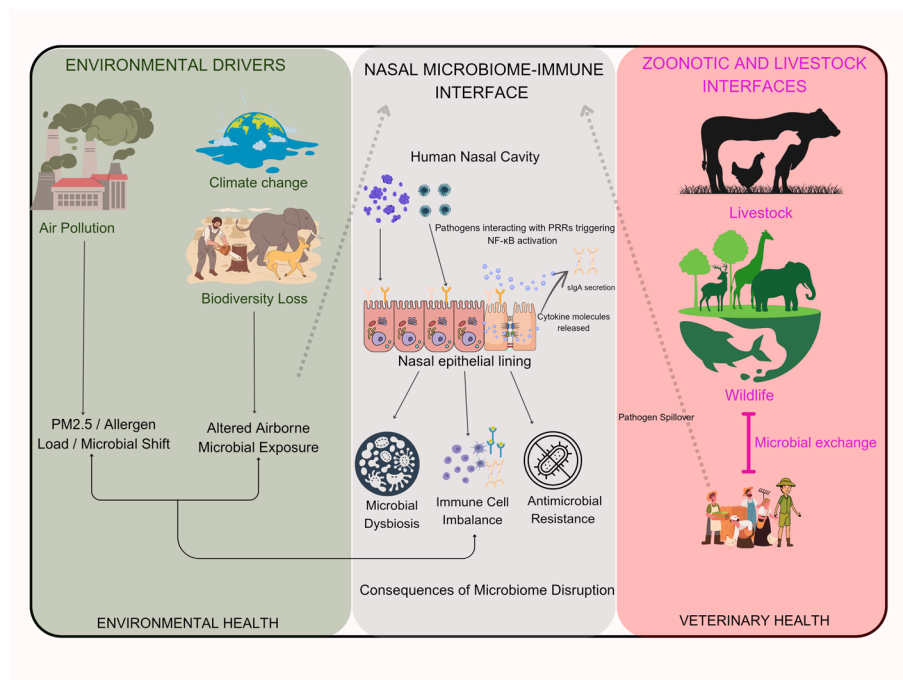


Fig. 1 Framework illustrating how environmental drivers and zoonotic interfaces influence the nasal microbiome and mucosal immunity. Airborne pollutants and zoonotic exposures modulate microbial communities within the nasal cavity, which interact with epithelial pattern recognition receptors (PRRs) and immune pathways, influencing cytokine production, sIgA secretion, and epithelial barrier integrity. This microbiome-immunology crosstalk enables the nasal cavity to function as an integrated One Health surveillance interface

during the 2024 outbreak [6]. In the context of AMR, hospital surface contamination has been linked to the presence of identical resistance genes found in the nasal swabs of patients [7]. Within the climate–health interface, exposure to PM_{2.5} and nitrogen dioxide (NO₂) alters nasal microbial composition in both infants and adults, shifts that predict an increased risk of asthma [8–10]. Integrating these insights positions the nose not only as a site of exposure but also as a planetary sentinel for converging health crises.

The term “nasal microbiome” encompasses several distinct anatomical niches, including the anterior nares, middle meatus, and nasopharynx, each characterised by unique microbial and immunological environments [11]. Defining the precise sampling site is therefore crucial for reproducibility. Moreover, the nasal microbiome’s intra- and inter-individual variability, driven by factors such as age, geography, exposure history, and host genetics, can obscure subtle sentinel signals [12, 13]. Longitudinal designs stratified by age groups and health status are essential for capturing temporal stability and determining the optimal sampling frequency for surveillance.

2 Validation roadmap and staged deployment

To translate the nasal-sentinel concept into practice, we propose a staged validation pathway beginning with small-scale clinical pilot studies. These pilots would assess whether pre-symptomatic shifts in microbial composition or mucosal immune markers precede the onset of clinical illness. Predictive performance refers to the model’s ability to distinguish between individuals who develop an infection and those who remain healthy, as measured by accuracy and lead-time compared to routine surveillance.

First, a retrospective re-analysis of existing nasal swab cohorts and occupational screening datasets should assess whether pre-symptomatic shifts in microbial composition or mucosal immune markers precede clinical cases (proof of concept). Second, controlled prospective pilots in two contrasting sentinel settings (an agricultural/livestock site and a high-pollution urban community) should estimate predictive performance and lead-time versus routine surveillance, and assess operational metrics such as turnaround time and false-alarm rate. Third, multi-site operational pilots would evaluate scalability, logistics, costs and governance before wider deployment. This staged approach balances scientific rigour with practical deployment and will allow thresholds, workflows and resource requirements to be refined iteratively from real-world data.

An illustrative pilot could recruit two sentinel sites (one rural livestock setting and one urban pollution hotspot), enrolling ~ 300 participants per site, with baseline measurements followed by twice-weekly nasal sampling over a defined high-risk period (Fig. 2). Core assays could include targeted metagenomic profiling for key taxa and AMR genes, real-time PCR or targeted assays for priority zoonotic pathogens, and multiplex mucosal cytokine and sIgA panels [14], alongside continuous environmental monitoring (PM_{2.5}, NO₂) and simple symptom logs. The primary outcome would be the ability of a prespecified composite nasal signature to predict laboratory-confirmed respiratory infections within a short lead time compared to routine surveillance. Secondary outcomes would include sample compliance, turnaround time, cost per alert and participant acceptability.



Fig. 2 Proposed prototype for nasal microbiome-based One Health surveillance

3 Operational triggers and decision rules

Operational decisions should be explicit but grounded in pilot-derived evidence. Rather than prescribing fixed numeric cutoffs, decision rules should be expressed in broader, implementable categories. For example, a sustained loss of microbial diversity over a predefined interval could be used as an early warning signal. Similarly, marked increases in key inflammatory or mucosal immune markers, such as cytokines or secretory IgA, relative to local baselines, may indicate an elevated risk. Additionally, the detection of zoonotic pathogen signatures or an increasing abundance of AMR genes within sentinel cohorts could serve as actionable triggers for targeted interventions. Alert thresholds and escalation pathways must be derived from pilot data and calibrated to local public health risk tolerance, resource availability, and acceptable false-alarm rates. Example actions tied to graduated alerts could include intensified diagnostic testing, targeted public advisories, occupational investigations, or veterinary stewardship measures, each of which is predefined in local standard operating procedures.

Any sentinel network must embed robust data governance and equity safeguards. Nasal genomic and immune data are sensitive; custodianship should rest with appropriate national or regional public-health authorities under transparent data-sharing agreements that include strong de-identification and restricted geolocation practices. Pilots must incorporate meaningful community engagement and co-design with affected groups (e.g., farmers, Indigenous communities, frontline workers) to ensure cultural consent, benefit-sharing (including local capacity building and the return of results), and relevance. Equity should guide deployment so that low-resource settings are not merely sampling sites, but rather beneficiaries and partners. We note the risk of medical colonialism and recommend a single, explicit statement and mitigation plan addressing power imbalances and local ownership in every project proposal.

4 Implementation & policy integration

It is essential to distinguish between microbial colonisation and disease causation. Most bacterial colonisation events are benign or even protective, and shifts in microbial diversity represent risk indicators rather than deterministic precursors of disease. Accordingly, any proposed interventions or surveillance triggers should be interpreted probabilistically, not prescriptively.

Implementation within a One Health framework will require cooperation among public health agencies, veterinary networks, and environmental monitoring programs to ensure the integration of data streams and equitable distribution of resources. Key steps include standardising sampling and laboratory protocols, integrating diverse data streams into interoperable platforms, and defining pre-agreed escalation pathways for detected signals. Protocol standardisation should support comparable analyses across humans, livestock and wildlife while permitting locally relevant adaptations.

Real-world enablers include international partnerships (e.g., WHO, Quadripartite agencies), investment in low-cost sampling kits and field-ready workflows, and the deployment of portable sequencing and rapid assay platforms (e.g., nanopore or targeted sequencing) where appropriate. Open, modular digital platforms that integrate microbiome, immunological, and environmental sensor data will enhance signal detection and local decision-making while safeguarding privacy and promoting equitable access.

Despite its promise, nasal microbiome analysis faces significant technical challenges. Samples are low in biomass and prone to human DNA contamination and environmental artefacts introduced during collection and processing. While decontamination protocols exist, they are costly and often inaccessible for large-scale surveillance in low-resource settings. Addressing these methodological limitations, through standardised sampling, negative controls, and affordable sequencing methods, will be essential for reproducibility and scalability.

5 Conclusion

The next pandemic may whisper in our noses before it ever reaches our lungs. Nasal microbiome surveillance, capturing real-time shifts at the intersection of environmental exposure, zoonotic pressure, and immune response, offers a powerful new pathway to intercept emerging zoonoses, silent AMR spread, and climate-driven disease. Yet as climate volatility accelerates spillover risks, passive monitoring is no longer tenable.

To meet this moment, three challenges must be confronted. First is governance: establishing ethical frameworks for the ownership and sharing of global nasal biometric data. Second is equity: ensuring that new tools such as acoustic therapy and sequencing technologies are deployed in ways that respect cultural contexts and avoid medical colonialism. Third is validation: rigorously testing novel interventions before they are widely implemented.

In response, we recommend that sentinel networks be piloted in high-risk ecosystems, including deforestation frontiers where zoonotic emergence is accelerating, urban livestock hubs where AMR amplification is a growing concern, and live animal markets that function as viral mixing vessels. At the same time, standardised nasal surveillance should be embedded within the Quadripartite's One Health Joint Plan, with alerts triggered when agreed biological thresholds are exceeded. While validation is still needed, embedding nasal microbiome surveillance into One Health frameworks offers a realistic path toward proactive global health security. Our noses, humble, universal, and exquisitely sensitive, are planetary stethoscopes waiting to be deployed. To heed their warnings is not just an act of vigilance; it is a defence of our shared future.

Author contributions

J.A. conceptualised and authored the nasal microbiome, immunology, acoustic therapy and One Health context, while F.B. provided contributions to the AMR findings. Both authors reviewed the manuscript.

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Data availability

No datasets were generated or analysed during the current study.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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