The hidden dimension of tuberculosis: non-human primate reservoirs and One Health strategies

Tuberculosis remains the world's leading cause of death from a single infectious agent, despite effective diagnostics and treatment. More than 10 million people develop tuberculosis each year, and over 1 million die, placing the disease among the top ten causes of death worldwide, according to WHO.[1] In their Health Policy paper (March, 2026), Coleman and colleagues[2] help to explain why tuberculosis continues to impose such a heavy burden. The authors describe the tuberculogenic environment, emphasising how structural determinants—including poverty, housing, nutrition, education, employment, and health-care system capacity—influence vulnerability to infection, disease progression, and transmission.[2] Infection with *Mycobacterium tuberculosis* is necessary but not sufficient for disease; social and environmental contexts largely determine individual and community outcomes.

However, an exclusively human-centred perspective overlooks a key dimension: the ecological and multi-species context of tuberculosis. The *Mycobacterium tuberculosis* complex (MTBC) comprises closely related pathogens capable of infecting humans and multiple animal species. Although host specificity exists, species such as *M tuberculosis*, *M bovis*, and *M orygis* can cross species barriers, enabling zoonotic and reverse zoonotic transmission.[3] Emerging evidence suggests that zoonotic tuberculosis is more widespread than previously recognised, with MTBC detected in domestic animals, wildlife, and free-ranging populations, although cross-species transmission dynamics remain poorly characterised owing to fragmented surveillance and inadequate molecular integration.[3,4]

Non-human primates are increasingly recognised as important spillover hosts. Reports from Asia and Africa have documented MTBC infections in macaques and vervet monkeys across free-ranging, captive, and research settings, underscoring the relevance of human–primate interfaces. Urbanisation, habitat encroachment, wildlife trade, and cultural practices amplify opportunities for bidirectional transmission, especially in densely populated areas with inadequate health-care access. As summarised in the appendix p 2, MTBC infections have been detected across diverse primate species and ecological contexts, highlighting the need to include non-human primates in integrated surveillance frameworks.[4]

Genomic studies have revealed strain variability and adaptive mutations that facilitate host switching, influencing virulence and transmissibility.[5] Integrating genomics with ecological and behavioural data can improve detection of transmission pathways and early warning systems. A One Health approach, linking human, animal, and environmental surveillance, is therefore essential. This approach includes targeted screening in high-contact populations, systematic wildlife and livestock monitoring, environmental sampling, and cross-sector training for health-care workers, veterinarians, and communities. Investments in next-generation vaccines for adolescents and adults, along with vaccination programmes for high-risk animal populations where feasible, could reduce reservoirs and curb spillover.

Reframing tuberculosis as a multi-species, socioecological disease transforms elimination strategies and underscores the need to address upstream social determinants, strengthen integrated surveillance across human and animal health systems, and map ecological hot spots of spillover and spillback. By combining microbiology, ecology, and public health, such strategies move beyond reactive responses towards proactive interventions essential for sustainable global tuberculosis control.

We declare no competing interests.

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