

REVERSE ZONOTIC DISEASE: HUMAN-TO-ANIMAL DISEASE TRANSMISSION AND ITS ONE HEALTH IMPLICATIONS

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Abstract

Public discussion of zoonotic disease nearly always runs in one direction: a virus jumps from a bat, a bird, or a pig into a person, and from there into the headlines. Far less attention is paid to the reverse traffic, in which humans pass their own pathogens back into animal populations. Reverse zoonosis, or zooanthroponosis, has been documented across viruses, bacteria, fungi, and parasites, with consequences that reach from zoo enclosures to national parks to industrial pig farms. This article traces the routes by which human pathogens reach animals, examines three well-studied cases, SARS-CoV-2 in mink and wildlife, methicillin-resistant *Staphylococcus aureus* in pig farming, and human respiratory viruses in wild apes, and considers what a One Health perspective demands of veterinarians, farmers, conservationists, and physicians alike. The pattern that emerges is consistent: wherever humans keep close, sustained contact with animals, whether through occupation, captivity, or habituation, our own microbes eventually cross the species line, sometimes with consequences as severe as those more readily associated with zoonotic spillover in the opposite direction.

Introduction

Ask a veterinary student to name a zoonosis and they will likely reach for rabies, brucellosis, or avian influenza: diseases that move from animal to human. Ask them to name a disease that moves the other way, and most will struggle. This gap in awareness is not a reflection of how rare the phenomenon is; a systematic review covering 2000 to 2022 found ninety-one published studies documenting human-to-animal pathogen transmission, with the United States, India, and Hong Kong reporting the largest number of events (Al Noman et al., 2024). It reflects, instead, an asymmetry in what has historically drawn research funding and public concern.

The term itself, reverse zoonosis or zooanthroponosis, describes any pathogen ordinarily reservoir in humans that establishes infection in another vertebrate species. An earlier and broader review, screening several thousand candidate titles down to fifty-six usable reports spanning three decades, found the recipients roughly balanced between wildlife, livestock, and

companion animals, with reports from every Continent except Antarctica (Messenger et al., 2014). The phenomenon is neither new nor geographically confined; it has simply been overshadowed by its better-known counterpart.

What changed the picture was the COVID-19 pandemic, which allowed a single pathogen's human-to-animal transmission to be tracked in close to real time, across species ranging from house cats to captive tigers to free-ranging deer. The result was less a discovery than a demonstration, in unusually sharp detail, of a pattern veterinary epidemiologists had already suspected.

How Human Pathogens Reach Animals

Three broad routes account for most documented cases.

The first is direct contact, the easiest to trace because it is the easiest to observe. A zookeeper with a cold breathes near the primates in her care; a farm worker's nasal staphylococci colonise the pigs he handles

daily; a park ranger with a common respiratory virus habituates a troop of gorillas that has, over years of tourism and research access, lost its wariness of humans.

The second route is environmental. Human sewage, inadequately treated, carries viable pathogens into rivers, soil, and groundwater that animals subsequently drink from or graze on. Where sanitation infrastructure is weak, this route becomes difficult to separate from direct contact, since the settlements that lack treatment facilities often sit closest to the water their livestock depend on.

The third is mediated by vectors or fomites, contaminated boots, veterinary equipment, or bedding carried between a human population and an animal one. This route is harder to document and consequently under-represented in the literature.

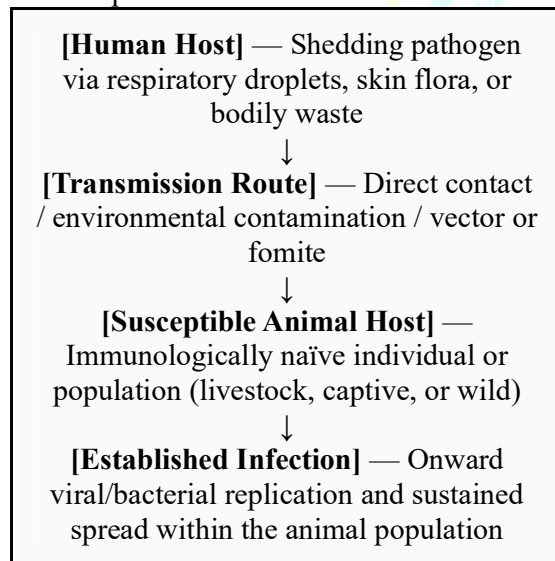


Fig. 1: Conceptual framework showing the four main stages of zoonotic spillover and pathogen establishment.

Three Documented Cases

SARS-CoV-2: an unusually well-tracked spillback

Between 2020 and 2022, genomic surveillance caught SARS-CoV-2 moving from humans into a remarkable range of species. On Dutch mink farms, the virus passed from workers into mink, circulated within the densely housed animals, and in several instances returned to humans carrying

mink-adapted mutations; Munnink and colleagues, sequencing virus from workers and mink on the same farms, showed unambiguous evidence of this farm-to-human-to-mink-to-human cycle (Munnink et al., 2021). At the Bronx Zoo, several tigers and lions developed a dry cough and loss of appetite in early 2020, with genomic sequencing linking their infections to an asymptomatic zookeeper (McAloose et al., 2020). Free-ranging white-tailed deer proved still more consequential: surveys across several American states found a substantial fraction of tested deer carrying the virus (Hale et al., 2022), and genomic analysis subsequently identified numerous independent spillover events from humans, rather than a single introduction followed by deer-to-deer spread (Kuchipudi et al., 2022). A sylvatic reservoir of this kind, sustained in a wild population with no realistic path to elimination, raises the possibility of continued viral evolution with periodic spillback into hunters and wildlife workers.

Livestock-associated MRSA: a resistant lineage born in humans

Where SARS-CoV-2 offers transmission caught almost as it happened, methicillin-resistant *Staphylococcus aureus* sequence type 398 offers a case reconstructed after the fact through genomics. Phylogenetic work by Price and colleagues traced ST398 to a human, methicillin-susceptible ancestor that, after moving into pig populations, acquired resistance to methicillin and tetracycline and lost the gene cluster it had used to evade the human immune system (Price et al., 2012). Having adapted to its new host, the lineage began moving back into people in close contact with pigs. A 2019 survey of thirty-two pig farms in southern Italy found MRSA colonising 21.6 per cent of farm workers, rising to 27.1 per cent on intensively managed farms and falling to zero on extensive, free-range operations; genomic comparison showed 94.1 per cent of the human isolates to be identical or near-identical to strains carried by pigs on the same farm (Pirolo et al., 2019).

The same lineage has caused documented bloodstream infections and, in two Italian farm workers, severe necrotising fasciitis. The organism had, in effect, completed a round trip: born in a human host, reshaped by livestock, and returned to a new generation of human carriers, this time resistant to first-line treatment.

Respiratory viruses in wild apes: habituation as a hazard

The third case involves free-living, endangered wildlife rather than domestic or captive animals, and the proximity that enables transmission is largely deliberate, built for tourism and research access. Mountain gorillas in Rwanda and chimpanzees in Uganda's Kibale National Park have both been the subject of long-running habituation programmes; the same closeness that funds conservation and

behavioural research has proved to be a route for human respiratory viruses. In December 2016 and January 2017, two chimpanzee communities in Kibale suffered simultaneous but genetically distinct outbreaks: one, caused by human metapneumovirus, killed twenty-five animals, 12.2 per cent of the affected community, while the other produced illness without any recorded deaths (Negrey et al., 2019). Human respiratory syncytial virus has separately been confirmed in Rwandan mountain gorillas during outbreaks of respiratory illness (Mazet et al., 2020), and an earlier case linked human metapneumovirus directly to the deaths of gorillas within a single family group (Palacios et al., 2011). For species numbering only in the low thousands, a single poorly timed outbreak is not a statistical curiosity; it is a measurable setback to population recovery.

Table 1. Summary of primary impacts across the three domains of the One Health framework.

Human Health	Animal & Ecosystem Health	Environmental Health
Re-infection with human pathogens modified in animal reservoirs; acquisition of antimicrobial-resistant strains (e.g., LA-MRSA ST398).	High mortality in naïve wildlife populations (e.g., great apes); establishment of intractable sylvatic reservoirs (e.g., white-tailed deer).	Contamination of soil, rivers, and groundwater via untreated sewage and agricultural runoff; dissemination of mobile resistance genes.

Human Health

The costs of reverse zoonosis to human health are less direct than its costs to animals, but not negligible. Livestock-associated MRSA illustrates the point precisely: an organism that gained its foothold in pigs has since caused documented infections, including severe ones, in the same farm workers who first carried its ancestor. Antibiotic stewardship in agriculture is therefore not only a matter of animal welfare; it shapes what happens when the same organisms return to human hosts.

Environmental Health

Environmental contamination underlies much of the indirect transmission route, and its significance is likely to grow.

Where sanitation infrastructure remains inadequate, the waterways that carry human waste also serve as drinking sources for wildlife and livestock; flooding, by disrupting sewage systems, makes this route more common rather than less.

Animal and Ecosystem Health

For wildlife populations already reduced to small, fragmented numbers, reverse zoonosis represents a threat disproportionate to the size of the pathogen involved. Diseases that cause mild, self-limiting illness in humans can produce double-digit mortality in a great ape community with no prior exposure and no acquired immunity. Conservation programmes built around habituating animals

to human presence face an uncomfortable trade-off: the access that funds anti-poaching patrols and research also opens a transmission route that would not otherwise exist.

Antimicrobial Resistance: A Reverse Zoonosis of Genes, Not Only Organisms

Livestock-associated MRSA demonstrates something broader than a single pathogen's journey between species: resistance genes, once established in an animal population, do not stay confined to the organism that first carried them there. Contaminated wastewater and manure allow resistance determinants to move between bacterial species independent of any single transmission event. Reducing antibiotic use in intensive animal husbandry therefore addresses not just animal health but one of the mechanisms by which resistance, once created, is sustained and redistributed across the human-animal interface.

Prevention Across Four Levels

Level 1: Individual Practice — Respiratory hygiene among animal handlers, PPE in high-density facilities, restricted visitor access to habituated wildlife during outbreaks of human respiratory illness, and routine screening of high-contact occupational groups such as swine farm workers and zoo staff.

Level 2: Farm Management — Addressing stocking density as a primary risk factor (e.g., Italian MRSA survey showing 0% colonisation in free-range vs 27.1% in intensive operations), establishing robust biosecurity protocols, and reducing routine antibiotic administration.

Level 3: Wildlife Management —

Implementing strict biosafety protocols for habituation/ecotourism programs (staff health screening, compulsory mask mandates, temporary tourism suspension during local outbreaks), and evaluating prophylactic wildlife vaccination against human pathogens for endangered species (Edwards et al., 2021).

Level 4: Integrated Policy & Surveillance

— Establishing integrated One Health genomic surveillance linking human, animal, and environmental isolates to identify spillback events early and transform anecdotal sightings into actionable epidemiological intelligence.

Conclusion

The direction of travel implied by the word "zoonosis" has shaped which diseases receive attention and funding; the reverse direction has, until recently, been left largely to specialists. The evidence assembled over the past decade, sharpened considerably by the surveillance capacity built during the COVID-19 pandemic, makes clear that this asymmetry was never justified by the underlying biology. Mink farms, pig barns, and habituated ape populations are not isolated curiosities; they represent the conditions, sustained close contact between humans and animals, under which pathogen exchange runs in both directions as a matter of course. Treating reverse zoonosis as an ongoing feature of the human-animal interface, rather than a footnote to the more familiar story of spillover, is a modest conceptual shift with a substantial practical payoff.

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