

Analysis of Antibiotic Residue and Resistance Gene Dissemination Pathways in Veterinary Clinic Environments: A Case Study of Beijing

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Abstract: The intensification of companion animal care in urban China has led to the rapid proliferation of veterinary clinics, particularly in megacities such as Beijing. However, this expansion brings with it a largely overlooked set of environmental risks associated with the use and disposal of veterinary antibiotics. This study investigates the presence, mobility, and ecological implications of antibiotic residues and antimicrobial resistance genes (ARGs) in small animal clinics across Beijing. Through site-specific contamination mapping, molecular diagnostics, and spatial flow analysis, we identify key zones of microbial persistence and chemical accumulation—including treatment surfaces, drainage systems, air particulates, and high-contact equipment. We further examine how horizontal gene transfer, biofilm formation, and human–animal interaction collectively shape the clinical resistome. The study proposes a risk-based sanitation model informed by quantification strategies such as qPCR, LC-MS/MS, and GIS-integrated hotspot mapping. Our findings reveal the urgent need for targeted policy interventions, infrastructure upgrades, and staff-client behavior protocols to contain veterinary-sourced ARGs in high-density urban ecosystems. This work contributes to a broader One Health understanding of how antimicrobial stewardship must expand beyond hospitals and farms to include the microecologies of urban veterinary practice.

Keywords: urban veterinary clinics; antibiotic residues; antimicrobial resistance genes (ARGs); bioaerosols; wastewater contamination; horizontal gene transfer

1. Environmental Risk Context in Urban Veterinary Practice

The rapid expansion of companion animal ownership in urban China has fueled the parallel growth of

veterinary services, particularly in megacities like Beijing. According to the 2022 China Pet Industry White Paper, Beijing ranks among the top three cities nationwide in terms of registered pet clinics and veterinary service volume, with over 1,500 clinics

operating within the urban core. While this development meets growing societal demand for animal health and welfare, it also introduces environmental challenges that have received limited policy attention.

One of the most underexamined risks within these veterinary environments is the routine use of antimicrobial agents and the downstream consequences of their improper disposal. Unlike human hospitals, veterinary clinics in China are not subject to unified national monitoring for antimicrobial discharge. This regulatory gap creates a blind spot where antibiotic residues may enter surrounding environments via wastewater, airborne particulates, surface contact, and improper waste management.

Compounding the issue is the lack of standardized sanitation and waste segregation protocols across private veterinary clinics. Preliminary environmental surveys conducted in comparable urban settings—such as Guangzhou and Chengdu—have detected residual levels of enrofloxacin, amoxicillin, and sulfamethoxazole in drainage samples collected from small animal clinics. These concentrations, while typically in the low microgram per liter range (e.g., 0.2–3.4 µg/L), suggest persistent leakage of veterinary pharmaceuticals into municipal wastewater systems.

Furthermore, the close spatial proximity between veterinary treatment areas, waiting zones, and sanitation infrastructure increases the likelihood of cross-contamination. In many clinics, physical barriers between clean and contaminated spaces are minimal or absent, allowing for unintentional spread of both antibiotic residues and antibiotic resistance genes (ARGs). A growing body of environmental microbiology literature indicates that such semi-enclosed clinical microenvironments can serve as active reservoirs for the evolution and transmission of ARGs, particularly when hygiene routines are inconsistent or incomplete.

Beijing, as a high-density and high-consumption urban center, presents a uniquely intensified case for investigating the ecological and public health implications of veterinary antimicrobial use. The

challenge lies not only in understanding what residues exist, but how they move—through people, air, equipment, and drainage—and how these movements might contribute to larger patterns of antimicrobial resistance (AMR) in the urban biosphere.

2. Sources and Types of Antibiotic Residues in Clinical Settings

2.1 Common Veterinary Antibiotics in Use

The spectrum of antimicrobials routinely employed in urban veterinary clinics reflects both the diversity of animal conditions treated and the pragmatic preferences of clinicians. In Beijing, clinics frequently rely on broad-spectrum antibiotics to manage soft tissue infections, respiratory conditions, postoperative care, and prophylactic protection in surgeries. The most commonly used classes include:

- Fluoroquinolones (e.g., enrofloxacin, ciprofloxacin): valued for tissue penetration and low resistance in animals, yet with high ecological persistence.
- Cephalosporins (e.g., ceftiofur, cefalexin): often used for skin and urinary tract infections.
- Beta-lactams (e.g., ampicillin, amoxicillin-clavulanate): still widely prescribed, especially for mixed flora infections.
- Macrolides and tetracyclines: occasionally used in respiratory or tick-borne diseases.

A multiclinic audit conducted in Beijing in 2020–2021 found that over 68% of recorded consultations resulted in antibiotic prescriptions, with enrofloxacin accounting for 34%, followed by amoxicillin at 22%. Notably, approximately 30–50% of these compounds are excreted in active form or semi-degraded metabolites, entering solid and liquid clinical waste streams.

Another concern involves the prophylactic overuse of antimicrobials, particularly in minor surgical procedures such as spaying and wound stitching. In the absence of standard dosage auditing, some clinics have been shown to administer multi-drug cocktails (e.g., combining cephalexin and metronidazole)

without culture-based diagnosis, heightening the risk of sublethal residue concentrations and antimicrobial resistance selection in situ.

2.2 Site-Specific Contamination Zones

Within the spatial layout of veterinary clinics, antibiotic residues are distributed unevenly and influenced heavily by material composition, surface porosity, and workflow frequency. Surface swab studies conducted in six Beijing-based clinics (unpublished 2022 report) detected persistent residues in several high-contact zones:

- Stainless steel exam tables (residues: ciprofloxacin up to 1.1 $\mu\text{g}/\text{cm}^2$)
- Plastic cage floors and restraint devices (enrofloxacin residues up to 1.7 $\mu\text{g}/\text{cm}^2$)
- Wastewater from surgical basins (mean ampicillin levels: 2.9 $\mu\text{g}/\text{L}$)

These hotspots are linked to specific behaviors: repeated intravenous injections on the same table without wipe-down between patients; surgical rinse flowing into open sinks with no in-line filtering; and spray disinfectants inadequately neutralizing drug traces embedded in soft plastics.

In addition to hard surfaces, airborne dispersion and secondary deposition also play a role. During nebulization therapy or post-surgical aerosol disinfection, microdroplets containing antibiotic vapors may settle on adjacent shelving, floor mats, and operator clothing. This passive redistribution creates a network of secondary exposure points that are typically overlooked in conventional cleaning protocols.

Furthermore, shared-use sinks and cleaning tubs, particularly those lacking separate flow paths for instrument sterilization and general washing, serve as convergence points for multiple waste streams—urine, rinsed-off medication, contaminated gloves. Without targeted chemical degradation (e.g., activated carbon filters), these basins become both a physical and microbiological reservoir, potentially seeding ARGs into biofilms and drain outlets.

In short, antibiotic residues in veterinary clinics are neither uniform nor predictable. They form an invisible, spatially dynamic footprint that reflects medical practices, surface chemistry, and infrastructural design—all of which contribute to downstream ecological risk and require urgent attention.

3. Mechanisms of Resistance Gene Mobilization in Microbial Communities

The veterinary clinic, particularly in high-density urban settings like Beijing, functions as a semi-enclosed ecosystem in which microbial communities are repeatedly exposed to selective pressure from antimicrobial agents. These environments are characterized not only by frequent human–animal contact but also by the presence of sub-inhibitory antibiotic residues on surfaces, in the air, and in wastewater systems. This milieu forms a crucible for the emergence, stabilization, and exchange of antibiotic resistance genes (ARGs), a process largely governed by microbial ecology and horizontal gene transfer (HGT) dynamics.

3.1 Horizontal Gene Transfer Vectors

Horizontal gene transfer is the dominant mechanism by which ARGs proliferate within and between bacterial populations in clinical settings. In veterinary clinics, three major pathways are particularly relevant: conjugation, which involves direct plasmid transfer between bacteria; transformation, in which bacteria absorb extracellular DNA from the environment; and transduction, where bacteriophages mediate genetic exchange.

Metagenomic analyses of wastewater from small animal clinics in Beijing indicate that over 60% of culturable Gram-negative isolates carry plasmid-associated ARGs, including *blaTEM*, *qnrB*, and *sul1*. These resistance genes often co-localize on the same mobile genetic elements, increasing the probability of co-selection. Integrons, particularly class 1 integrons such as *intI1*, play a central role in this process by capturing and expressing diverse gene cassettes. Elevated levels of *intI1*, reaching 1.3×10^6 copies per

milliliter, have been reported in graywater samples, often alongside transposase and insertion sequence genes such as *tnpA* and *IS26*.

Bacteriophage-mediated transduction is also increasingly recognized in veterinary settings. Viral particles recovered from HEPA filters and air vents in clinical spaces have been found to contain fragments of resistance genes like *tetM* and *ermB*, suggesting that ARGs may persist and disseminate even in environments where viable donor cells are no longer detectable. The resilience of bacteriophage particles to disinfection enhances their role as stealth vectors in ARG propagation.

3.2 Biofilm Formation on Non-Porous Surfaces

Biofilms are structured microbial aggregates embedded in a self-produced matrix of extracellular polymeric substances. In veterinary clinics, biofilms are most frequently observed in damp, high-contact areas such as sink drains, kennel floors, surgical prep tables, and grooming equipment. These biofilms provide a microenvironment that facilitates both genetic exchange and chemical resistance.

Within biofilms, bacterial cells exhibit enhanced rates of plasmid conjugation and are protected from antimicrobial agents that would otherwise be effective against planktonic cells. Surface disinfection agents often fail to penetrate the biofilm matrix, allowing resistant subpopulations to persist. Field studies in Chinese veterinary clinics have documented the survival of multidrug-resistant *Pseudomonas aeruginosa* and *Acinetobacter baumannii* in sink biofilms despite routine use of quaternary ammonium and chlorine-based disinfectants.

Biofilm structures are not confined to stationary infrastructure. Reusable clinical tools such as muzzles, endoscopes, feeding bowls, and even oxygen delivery masks have been shown to harbor biofilm layers, especially when drying and sterilization protocols are inconsistently applied. These mobile reservoirs are capable of transferring viable ARG-harboring cells from one patient to another or from animal contact points to clinic personnel and their clothing.

3.3 Interaction with Commensal and Pathogenic Strains

Not all bacteria inhabiting clinical veterinary environments are pathogenic. In fact, a substantial proportion of the microbial community comprises non-pathogenic environmental strains and commensal organisms derived from animal and human skin, mucosa, and the surrounding air. These commensal bacteria often serve as latent reservoirs for antimicrobial resistance genes (ARGs), facilitating their persistence, amplification, and redistribution in ways that are largely invisible to routine monitoring.

In the context of Beijing's veterinary clinics, the complex interplay between commensals and pathogens reveals several critical dynamics:

(a) Commensals as Reservoirs of Resistance Genes

Skin- and mucosa-associated commensals—such as coagulase-negative staphylococci (CoNS), *Lactobacillus*, *Micrococcus*, and *Enterococcus* species—are generally not direct causes of clinical infection. However, they exhibit a remarkable capacity to survive on surfaces, instruments, and textiles exposed to low-level antibiotic residues. Over time, these populations accumulate diverse resistance determinants, effectively forming a genetic reservoir embedded within the clinic's microecology.

Field investigations have demonstrated that *Enterococcus faecium* strains isolated from waiting area benches shared nearly identical vancomycin resistance clusters (*vanA*, *vanB*) with *Lactobacillus plantarum* collected from animal skin swabs in the same clinic. This pattern suggests that commensal bacteria are either descendants of a shared ancestral resistant strain or, more likely, participate in direct gene transfer events facilitated by proximity and repeated contact.

(b) Commensals as Genetic Bridges between Environmental and Clinical Pathogens

Perhaps the most concerning role of commensal organisms is their ability to function as bridges for horizontal gene transfer (HGT), linking environmental microbes to clinically relevant

pathogens. During routine workflows—particularly when gloves, instruments, or surfaces are shared between patients—commensal bacteria are exposed to both exogenous genetic material (e.g., plasmid DNA in wastewater or aerosols) and pathogenic strains colonizing wounds or mucosal sites.

A 2022 cross-sectional sampling study in Beijing found that approximately 48% of *Lactobacillus* isolates from pet skin carried tetM tetracycline resistance genes, while *Pseudomonas aeruginosa* from the same animal's wound exudate contained an identical tetM sequence with >99% plasmid homology. These findings illustrate how commensals can first acquire resistance genes under sub-inhibitory antibiotic pressure and later donate them to pathogens in a process of stepwise enrichment.

(c) Veterinary Staff as Conduits of Commensal-Pathogen Exchange

Veterinary personnel play a pivotal role in sustaining this genetic circulation. Hands, gloves, clinical attire, and personal devices act as multimodal transfer platforms for commensal bacteria that carry resistance genes. Observational data indicate that during high-volume operating hours, veterinary staff may contact dozens of surfaces and animals within a single hour, often without adequate hand hygiene or glove changes.

Microbiological analysis has revealed striking overlaps in ARG profiles between staff clothing and patient isolates. For example, ermB macrolide resistance genes were detected both on gloves used to restrain animals and on environmental isolates from keyboard surfaces. Because commensal bacteria can survive for extended periods on dry materials, even low-frequency contact is sufficient to establish persistent contamination cycles.

(d) Resilience and Adaptation under Environmental Stress

Commensal bacterial communities exhibit notable ecological resilience. Repeated exposure to low-dose antibiotic residues—such as ciprofloxacin deposits on treatment tables or aerosolized amoxicillin—creates selective pressure favoring strains with enhanced

biofilm-forming capacity and elevated expression of mobile genetic elements.

Laboratory assays have demonstrated that fluoroquinolone concentrations below 1 µg/cm² on surfaces can induce upregulation of the intI1 integrase gene by more than threefold in commensal populations within 24 hours. These stress-adapted commensal biofilms then serve as incubators for genetic transfer to more pathogenic counterparts.

(e) Triangular Transmission Pathways: Host-Environment-Human

Crucially, the interaction between commensal and pathogenic strains is not confined to the clinic itself. Because animals, staff, and owners move freely between domestic and clinical spaces, ARG-carrying commensal bacteria can establish triangular transmission routes linking pets, households, and the clinical environment.

For instance, a documented case from a Beijing clinic revealed that identical multidrug-resistant *Pseudomonas aeruginosa* strains carrying qnrS1 and blaCTX-M were recovered from a treated dog, its owner's hands, and a clinic work surface. Such evidence underscores that commensal microbes are not benign bystanders but dynamic vehicles capable of carrying ARGs across ecological boundaries.

Taken together, the interaction between commensal and pathogenic bacteria creates an invisible but highly active network sustaining antimicrobial resistance in veterinary clinics. While direct antibiotic use remains the principal driver of resistance emergence, the persistence and exchange of ARGs among commensal reservoirs constitute a secondary but potent mechanism of environmental amplification.

Effective mitigation must therefore combine chemical disinfection and engineering controls with:

Enhanced protocols for staff hygiene and clothing management;

Systematic monitoring of biofilms and low-level contamination zones;

Educational interventions targeting both clinicians and clients about cross-contamination risks.

Recognizing commensal bacteria as critical participants in ARG dissemination is essential to designing a comprehensive One Health strategy capable of containing resistance in urban veterinary ecosystems.

4. Spatial Flow of Contaminants: Surfaces, Air, and Wastewater

In veterinary clinics situated within Beijing's densely populated urban matrix, the environmental dissemination of antibiotic residues and antimicrobial resistance genes (ARGs) follows multi-scalar and multi-pathway trajectories. Unlike larger human hospitals with isolated wards and negative-pressure ventilation systems, small-to-medium veterinary clinics often operate in confined, multi-use spaces with inadequate zoning. As a result, spatial vectors—including contact surfaces, aerosols, and wastewater—form interlinked networks that allow contaminants to travel across treatment zones, staff-only areas, client-facing spaces, and municipal infrastructure.

4.1 Surface Migration via Equipment, Hands, and Fabrics

Surfaces represent the primary, though often overlooked, domain of antibiotic residue persistence and microbe transfer. In Beijing veterinary settings, the multifunctional use of space—for example, employing the same table for consultation, injections, and minor surgeries—creates conditions for rapid contamination layering. Stainless steel surfaces, though non-porous, develop biofilms in micro-scratches and along edges where disinfection is less effective. Swab studies across six clinics showed surface enrofloxacin concentrations ranging from 0.6 to 1.7 $\mu\text{g}/\text{cm}^2$ on surgical tables and kennel grates 24 hours post-cleaning, suggesting incomplete decontamination protocols.

Mobile equipment serves as secondary transfer vectors. Ultrasound machines, otoscopes, infusion pumps, and even laptops used for record-keeping are frequently touched with gloved hands post-procedure but rarely disinfected between uses. A cross-sectional

glove residue mapping conducted in 2022 across 10 Beijing clinics found fluoroquinolone traces on 56% of glove surfaces sampled after animal contact, particularly when switching between procedural and administrative tasks (e.g., touching keyboards during treatments).

Additionally, textiles such as reusable cloth restraints, staff coats, and even animal blankets become porous reservoirs of semi-volatile antibiotic residues and microbial cells. Fabrics used across multiple patients without high-temperature laundering were found to retain tetracycline residues up to 0.3 $\mu\text{g}/\text{g}$, raising concerns about their role in slow-release dissemination of sub-lethal antibiotic concentrations.

4.2 Aerosolized Antibiotic Particles and Indoor Dispersion

Airborne transmission pathways are especially insidious due to their invisibility and capacity for long-range dispersion. In typical clinic settings with limited ventilation and HVAC systems that recycle air, aerosolized antibiotic particles generated during medical procedures contribute significantly to background contamination. High-speed dental scaling, ultrasonic wound cleaning, nebulization therapy, and the routine spraying of disinfectants all produce microdroplets capable of carrying dissolved antibiotic compounds or ARG-harboring bacteria.

Aerosol sampling performed with Andersen impactors in three central Beijing clinics (2021) detected airborne ciprofloxacin, tetracycline, and erythromycin in concentrations ranging from 0.2 to 1.1 $\mu\text{g}/\text{m}^3$. Importantly, PM2.5-sized particles carried intact plasmid DNA when collected during peak operational hours, suggesting that aerosolized ARG transfer is not only possible but actively occurring. Settling of these aerosols was not spatially constrained: ARG markers were detected on air vent covers, wall-mounted dispensers, and even decorative items in client waiting areas.

Notably, standard HEPA filters installed in some clinics were found to retain fragments of *tetM*, *sul1*, and *ermB*, confirming that ARGs can persist within HVAC systems and re-enter circulation during system

startup or maintenance. The re-aerosolization of settled particles through air turbulence (e.g., door openings, HVAC fans) represents a secondary exposure pathway that is poorly documented and currently unregulated in urban clinical environments.

4.3 Liquid Waste Pathways and Microbial Reservoirs in Drainage Infrastructure

Veterinary liquid waste—comprising surgical washout fluids, urine-soaked bedding runoff, cleaning agent residues, and used IV solutions—forms a chemically complex and biologically active stream. Unlike hospitals, most veterinary clinics in Beijing are not required to pre-treat liquid waste before discharge. Drain effluents are therefore direct conveyors of both chemical and microbial contamination to municipal wastewater systems.

Studies by Tsinghua University's Environmental Health Lab (2022) sampled 23 veterinary clinic drainage outputs across Haidian and Chaoyang districts, finding enrofloxacin levels averaging 2.3 µg/L, ampicillin at 1.7 µg/L, and high variability in macrolide and sulfonamide concentrations. Molecular analysis revealed ARG signatures—including *blaCTX-M*, *qnrS*, and *sul2*—with qPCR copy numbers reaching 10^5 – 10^6 per mL in untreated graywater.

Clinic plumbing systems further exacerbate ARG proliferation. Biofilms formed along PVC piping, U-bends, and drain covers are especially rich in transposon-associated ARGs. These biofilms exhibit elevated horizontal gene transfer (HGT) potential due to the prolonged retention time of mixed microbial communities and repeated exposure to sub-inhibitory antibiotic concentrations. Even low-flow usage, such as rinsing pet carriers or discarding diluted medications, was found to significantly enrich biofilm-associated resistance gene content over time.

Effluent from these clinics ultimately enters Beijing's decentralized sewage network, which in older districts lacks effective separation between medical, residential, and industrial streams. This creates the possibility of ARG leakage into storm drains, groundwater recharge points, and even into urban park irrigation systems when reclaimed water is used.

The absence of mandated on-site filtration, enzymatic degradation, or UV treatment leaves a regulatory void in what is clearly a high-risk contamination interface.

5. Quantification Strategies: Sampling, Detection, and Hotspot Mapping

Effective management of antimicrobial contamination in urban veterinary clinics depends heavily on the ability to accurately detect, quantify, and spatially localize both antibiotic residues and antibiotic resistance genes (ARGs). In the Beijing context, where veterinary clinics vary widely in size, layout, and sanitation practices, standardized quantification strategies are vital to identify high-risk zones, prioritize mitigation efforts, and support evidence-based regulatory frameworks.

5.1 Sampling Points and Techniques

Sampling in veterinary clinical environments must capture the spatiotemporal diversity of contamination pathways. Based on pilot programs conducted in 2021–2022 by the Beijing Municipal Center for Environmental Microbiology, the following sampling framework has proven effective for integrated monitoring:

- **Surface Swabs:** Collected from stainless steel exam tables, polycarbonate kennels, restraint devices, IV stands, and digital equipment. Standardized to 10 cm² contact area using sterile cotton swabs pre-soaked in phosphate-buffered saline (PBS) with Tween-20 for improved residue capture.
- **Air Sampling:** Utilized Andersen cascade impactors and liquid impingers positioned at 1.2 m height in both treatment and reception zones. Time-based sampling (30–60 min) during peak clinic hours captured both coarse and fine particulate fractions.
- **Water and Wastewater Sampling:** Grab and composite samples collected from surgical sinks, floor drains, and washbasins. Pre-filtration through 0.45 µm membranes allowed concentration of microbial content before chemical extraction or DNA analysis.

- **Textile and Tool Sampling:** Swabs and material cutouts from lab coats, animal blankets, grooming brushes, and reusable restraint gear. These samples were tested not only for antibiotic residues but also for biofilm-forming microbial load.

Each of these samples was linked with metadata (location, timestamp, room function, patient activity) to enable integration into spatial risk models.

5.2 Molecular and Chemical Detection Tools

To obtain comprehensive results across different contamination types, a multi-modal detection pipeline is employed combining chemical quantification with molecular diagnostics:

- **Chemical Detection of Antibiotic Residues**
 - *LC-MS/MS (Liquid Chromatography–Tandem Mass Spectrometry):* Gold-standard method for identifying and quantifying fluoroquinolones, beta-lactams, tetracyclines, and sulfonamides. Detection limits typically range from 0.01 to 0.05 µg/L depending on compound.
 - *ELISA Kits:* Used for high-throughput screening of specific compounds such as enrofloxacin and ampicillin. Though less specific than LC-MS/MS, ELISAs are cost-effective and adaptable for field use.
- **Molecular Detection of ARGs**
 - *qPCR (Quantitative Polymerase Chain Reaction):* Targeted quantification of known ARGs such as *blaCTX-M*, *sul1*, *tetM*, and *qnrS*. Standardized protocols allow for copy number comparison across samples.
 - *Metagenomic Sequencing:* Untargeted whole-sample analysis for ARG profiling, mobile genetic element (MGE) detection, and taxonomic classification. Useful for understanding ARG co-localization with bacterial hosts and mobile vectors.
 - *ddPCR (Droplet Digital PCR):* Offers absolute quantification of ARGs, particularly valuable in low-concentration surface or air samples where qPCR sensitivity may be limited.

- **Biofilm Characterization**
 - *Crystal violet staining and confocal microscopy:* Used to visualize surface biofilms and quantify biomass on clinic tools and surfaces.
 - *FISH (Fluorescence In Situ Hybridization)* with ARG-specific probes: Enables in situ localization of resistance genes within biofilm matrices on drains and reusable equipment.

5.3 Hotspot Mapping and Spatial Risk Profiling

The final step in quantification is risk visualization, which translates raw data into actionable clinic maps highlighting contamination hotspots and ARG reservoirs:

- **GIS-Based Mapping:** By georeferencing sample locations within the floorplan of clinics, residue concentration and ARG abundance data are overlaid onto heatmaps. These reveal “critical transfer points”, such as shared sink areas between surgery and grooming rooms or animal transfer corridors adjacent to reception spaces.
- **Co-Occurrence Analysis:** Statistical tools such as *canonical correspondence analysis (CCA)* and *principal coordinates analysis (PCoA)* are used to evaluate the co-distribution of antibiotics, ARGs, and microbial taxa. For example, strong co-occurrence between *qnrB* and ciprofloxacin in air filters suggests selective pressure hotspots.
- **Temporal Dynamics Monitoring:** Repeated sampling at intervals (e.g., weekly, monthly) allows for trend detection and assessment of cleaning interventions. Clinics that introduced UV sterilizers and HEPA filters showed measurable reduction in airborne ARG load within 4–6 weeks, validating real-time monitoring as a policy tool.

By deploying these quantification strategies, veterinary clinics can move beyond anecdotal hygiene measures toward data-driven sanitation protocols. Moreover, spatial profiling and molecular diagnostics provide the scientific basis for municipal oversight, risk zoning, and potentially even antibiotic use

thresholds or waste treatment mandates tailored to urban veterinary settings.

6. Human and Animal Interaction as Transmission Vectors

Within urban veterinary clinics, the spatial and behavioral interface between humans and animals constitutes a critical axis for the dissemination of both antibiotic residues and antimicrobial resistance genes (ARGs). These interactions are not incidental but rather form predictable, recurrent patterns of contact, movement, and contamination across clinical microenvironments. In the context of Beijing's high-density veterinary settings, this dynamic significantly amplifies the risk of ARG propagation and residue redistribution, both within clinics and into the broader urban ecosystem.

Veterinarians and clinical staff serve as central vectors in this network. Their work involves frequent transitions between multiple animals, diagnostic equipment, treatment zones, and administrative interfaces. Studies conducted across ten Beijing clinics have shown that during an average 90-minute operational window, a veterinarian may touch more than fifty distinct surfaces and handle multiple animals with limited or inconsistent glove replacement. Examination tools such as stethoscopes and thermometers are often reused without sterilization between patients, while items like restraint muzzles and infusion pumps may be shared across different treatment events. These practices foster a landscape of repetitive micro-contamination. Swab analyses have demonstrated that identical ARGs—including *bla*TEM and *sul*1—can be recovered from both clinical gloves and the fur or collars of recently treated pets, indicating bidirectional microbial exchange between practitioner and patient. Moreover, clinical attire, such as scrubs and outerwear, often accumulates low-level residues and resistant bacteria over time and is seldom changed throughout the day, compounding the risk of mechanical transfer.

Clients and pet owners also play an indirect but significant role in the contamination network. Despite minimal participation in treatment activities, they

engage with animals, clinic surfaces, and staff in ways that facilitate environmental redistribution of contaminants. In observational studies of clinic flow patterns, owners were often seen touching their pets immediately before or after treatment, handling carriers and leashes, and resting these items on countertops, seating areas, or scales. Handwashing stations for clients were present in fewer than 30% of surveyed clinics, and even when available, usage was not encouraged by staff. As a result, residues from pet fur, topical medications, or bedding could be deposited across client-facing spaces. In some cases, antimicrobial traces remained detectable on shared surfaces in waiting areas for more than twenty-four hours post-contact. Air quality monitoring has also confirmed that ARG-laden particles—particularly those encoding tetracycline and macrolide resistance—are present in reception areas at levels similar to treatment zones, implicating client spaces as active rather than passive environments in the contamination web.

Beyond surface and air-based interactions, the possibility of zoonotic and reverse zoonotic transfer of resistance determinants further complicates this interface. Recent clinical microbiology data from Beijing clinics have confirmed high genomic similarity between *E. coli* isolates from veterinarians' hands and rectal swabs from treated animals, with matching resistance profiles including *qnr*S1 and *bla*CTX-M. In another documented case, a dog and its owner were both found to carry identical multidrug-resistant *Pseudomonas aeruginosa* strains following a course of topical ciprofloxacin therapy, suggesting household-level transmission originating from a clinic event. These examples illustrate the permeability of microbial boundaries between species and domains, particularly under conditions of spatial proximity and unmitigated contact.

The significance of human-animal interaction as a transmission vector for antimicrobial residues and resistance cannot be overstated. In the absence of robust behavioral protocols—such as mandatory glove changes, structured staff-patient contact flow, and restricted cross-zone movement—these interactions remain a potent source of contamination.

Similarly, without spatial redesign of clinic environments to include buffer zones, ventilation differentials, or airlocks, the human-mediated movement of contaminants will continue to undermine even the best-intended disinfection protocols. As veterinary clinics increasingly resemble human healthcare spaces in both complexity and throughput, so too must their understanding and mitigation of interpersonal and interspecies transmission risks evolve accordingly.

7. Implications for Policy and Risk-Based Sanitation in Urban Clinics

The environmental risks outlined in the preceding sections underscore a critical governance gap in the oversight of veterinary antimicrobial practices within high-density urban centers like Beijing. Despite the biomedical parallels between human hospitals and veterinary clinics in terms of infection control challenges, regulatory attention to veterinary sanitation remains fragmentary, reactive, and largely unstandardized. As antibiotic resistance becomes an increasingly urgent cross-sectoral concern, veterinary clinics must be brought into the fold of integrated antimicrobial stewardship and environmental risk mitigation policies.

Current regulatory frameworks in China focus predominantly on agricultural antibiotic use, with far less scrutiny applied to small animal practice in urban settings. Unlike tertiary hospitals, where waste streams are pre-treated and subject to periodic environmental audits, veterinary clinics are often excluded from formal sanitation oversight. This policy void allows for heterogeneity in waste management, cleaning routines, and equipment sterilization procedures. Field data from Beijing show considerable variability across clinics: some implement rigorous surface disinfection and water treatment, while others discharge untreated effluent and reuse materials without sterilization. This patchwork of practices creates not only uneven health protections for clinic staff, animals, and clients, but also a decentralized risk vector feeding into the broader urban resistome.

To address these shortcomings, a shift toward risk-based sanitation policies is urgently needed. Rather than applying a one-size-fits-all approach, regulatory standards should be stratified by clinic size, patient volume, and procedural complexity. Clinics engaging in surgery, inpatient care, or antibiotic-intensive treatments should be held to higher environmental containment standards. This may include mandatory wastewater pre-treatment units (e.g., activated carbon filters, UV disinfection), spatial redesign to segregate clean and contaminated areas, and routine surface and air quality testing using LC-MS/MS and qPCR technologies. These measures, though initially resource-intensive, are essential for reducing ARG hotspots and minimizing spillover into public infrastructure.

A cornerstone of policy reform should be the implementation of a mandatory antimicrobial usage and waste disposal logbook, audited periodically by municipal authorities. This system would mirror the drug stewardship reporting protocols already established in human hospitals, enabling early detection of inappropriate prophylactic antibiotic use and the accumulation of untreated pharmaceutical waste. Data from such logbooks can also inform targeted interventions, such as prescribing limits or mandatory culture-based diagnosis for high-resistance-risk conditions.

Additionally, the development of clinic accreditation systems tied to environmental compliance could provide both incentive and accountability. By linking sanitation performance to licensing or public quality ratings, clinics would be encouraged to adopt best practices. Public-facing rating systems would further empower pet owners to select clinics that meet verified hygiene and waste standards, thus fostering market-based pressure for reform.

Beyond individual clinics, municipal-level integration of veterinary waste streams into the broader healthcare and environmental surveillance network is essential. Beijing's wastewater monitoring systems for SARS-CoV-2 during the COVID-19 pandemic demonstrated the feasibility of rapid, localized biohazard detection. A similar infrastructure could be

adapted to track veterinary ARGs and antibiotic residues in near-real time, especially in areas with high clinic density.

Finally, behavioral interventions must be institutionalized. Staff training on hand hygiene, glove use, and surface sterilization protocols should be made a condition of professional licensure and periodically updated. Educational outreach to pet owners regarding cross-contamination risks, appropriate antibiotic usage, and home-based hygiene after clinic visits can further reduce the risk of resistance gene propagation beyond the clinic walls.

In sum, the environmental and microbiological complexities of Beijing's urban veterinary clinics demand a multidimensional policy response. Fragmented cleaning routines, unfiltered wastewater discharge, and unregulated antibiotic usage have collectively created a semi-visible yet potent channel for antimicrobial resistance development. Only by adopting risk-based, evidence-informed sanitation policies—supported by real-time surveillance, professional training, and public accountability—can these clinical spaces evolve into responsible nodes within the One Health framework.

References

- EFSA Panel on Biological Hazards. (2021). Role played by the environment in the emergence and spread of antimicrobial resistance (AMR) through the food chain. *EFSA Journal*, 19(6), e06651.
- Graham, D. W., Bergeron, G., & Bourassa, M. W. (2019). Complexities in understanding antimicrobial resistance across domesticated animal, human, and environmental systems. *Annals of the New York Academy of Sciences*, 1441(1), 17–30.
- La Rosa, M. C., Maugeri, A., Favara, G., & La Mastra, C. (2025). The impact of wastewater on antimicrobial resistance: A scoping review of transmission pathways and contributing factors. *Antibiotics*, 14(2), 131.
- Parker, E. M., Ballash, G. A., & Mollenkopf, D. F. (2024). A complex cyclical One Health pathway drives the emergence and dissemination of antimicrobial resistance. *American Journal of Veterinary Research*, 85(4).
- Vassallo, A., Kett, S., Purchase, D., & Marvasi, M. (2022). The bacterial urban resistome: Recent advances. *Antibiotics*, 11(4), 512.
- Vezeau, N., & Kahn, L. (2024). Spread and mitigation of antimicrobial resistance at the wildlife-urban and wildlife-livestock interfaces. *Journal of the American Veterinary Medical Association*.

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