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Zoonotic risks of household pets among children in urban and periurban Iraq: Antimicrobial resistance insights

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Abstract

Pet-associated zoonotic diseases in children represent a public health concern, particularly in resource-limited settings. The purpose of this study was to measure the level of prevalence of the carriage of zoonotic pathogens among children living with domestic pets, to determine the most common pathogenic agents, to characterize the distribution of antimicrobial resistance, and to define the major risk factors that predispose to transmission. Stool, nasal swab, skin swab, and blood samples were collected from children, while rectal swabs, fecal samples, fur/feather swabs, and nasal swabs were collected from pets. Microbiological culture, PCR-based identification of the pathogen, MALDI-TOF mass spectrometry, and broth microdilution antimicrobial susceptibility testing were done. Independent risk factors were identified using logistic regression analysis. Zoonotic pathogen prevalence was 48.4% in dog-owning children (n=124), 52.0% in cat-owning children (n = 98), 38.8% in bird-owning children (n = 67), and 14.6% in control children (n = 89), all groups $p<0.001$ vs. control. Toxocara spp., *Campylobacter* spp., *Salmonella* spp., *Pasteurella multocida* and *Chlamydia psittaci* (the latter detected exclusively in the bird group, at 11.9%) were the most common pathogens. *Campylobacter* exhibited 22.6% multidrug resistance. Unvaccinated pets (aOR = 4.19), child age less than 5 years (aOR = 3.65), and lack of handwashing (aOR = 3.07) were independent risk factors. Of total annual cases, 39.3% occurred during summer. The fact that the antimicrobial resistance rates are high highlights the necessity of diverse One Health surveillance and public health programs such as compulsory vaccination of pets, hygiene training, and regular veterinary check-ups.

Introduction

Zoonotic infections, which can be transmitted between animals and humans, are estimated to cause 60% of all known human infectious diseases and 75% of all emerging infectious diseases worldwide over the past thirty years (1, 2). Among the myriad animal-human interfaces by which such pathogens may be spread, household pets have a singularly close and unique niche. In contrast to wildlife contacts, companion animals share living

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spaces with their owners, which poses a sustained opportunity to experience direct contact, aerosolization of secretions, and environmental contamination (3, 4).

There are various reasons why children are disproportionately susceptible to pet-associated zoonotic infections. They are immunologically naive, and their stage of development predisposes them to hand-to-mouth actions, and they have more direct contact with animals than adults do (5, 6). Globally, pets are kept in about 57 percent of homes, and in the Middle East, pet ownership is increasing rapidly, even in Iraq, as urbanization and socioeconomic development advance (7, 8). However, the prevalence of pet-related zoonotic diseases among Iraqi children has been hardly researched, which is a serious gap in knowledge among pediatric and community health professionals. Enteric bacterial infections (*Campylobacter*, *Salmonella*, *Yersinia*), parasitic infections (*Toxocara*, *Cryptosporidium*, *Giardia*), respiratory pathogens (*Chlamydia psittaci* of birds), dermatological infections (*dermatophytes*, *Staphylococcus aureus*), and bite-associated bacterial infections (*Pasteurella multocida*) are among the key zoonotic threats associated with household pets (9, 10). The development of antimicrobial-resistant types, especially MRSA and fluoroquinolone-resistant *Campylobacter*, has introduced a critical aspect to these issues (11-14). Iraq represents a particularly important setting in the context of such research. There has been a significant urbanization (>70% urban) in the country, and veterinary services such as pet vaccination programs are not evenly distributed, and public awareness of the zoonotic risk posed by pets is low (15, 16). Previous research conducted in neighboring countries such as Turkey, Iran, and Jordan has recorded high levels of *Toxocara* seroprevalence and *Campylobacter* shedding. However, it has not fully characterized the range of pathogens present in various pets, nor has it profiled antimicrobial resistance within the same households (17, 18). The main aims of this study were: (i) to establish the prevalence of a comprehensive panel of zoonotic pathogens among children living with dogs, cats, or birds compared with a control group without pets; (ii) to characterize antimicrobial resistance profiles of bacterial isolates; (iii) to determine the seasonal distribution of pathogen detection; (iv) to identify independent risk factors for zoonotic pathogen acquisition; and (v) to describe the clinical manifestations associated with detected pathogens.

Materials and Methods

Study Design and Setting

This was a prospective, cross-sectional analytical study carried out in all five administrative districts of Mosul city (Al-Rashidiya, Al-Zuhour, Al-Dawasa, Nabi Younis, Al-Yarmouk) in Nineveh Governorate, Iraq (estimated population 1.8 million) between January and December 2025. Districts were purposefully selected to represent a range of urban and peri-urban residential environments and socioeconomic statuses and housing densities. Data collection was done at the same time across all districts with trained field teams made up of a nurse, a veterinary technician, and a data enumerator. Household recruitment was undertaken through the primary healthcare center (PHC) registries in each district, with community-based recruitment in high pet-ownership neighborhoods, as determined by the preliminary door-to-door survey in November-December 2024. Households were called by phone or visited in person, with eligibility confirmed at a preliminary screening appointment, prior to enrolment.

Population, Eligibility Criteria, and Participant Recruitment

The target groups were children aged 2-12 years who lived in Mosul and who had a close contact with at least one household pet daily. Four study groups were established: pet groups (dog owner, cat owner, bird owner), and a control group (no pet). Households with more than one pet species were assigned to the group of their primary pet species (the one that the parent reported as the species that was most connected daily) and excluded from other group analyses. The inclusion criteria were: (i) children aged 2–12 years; (ii) living with the same

pet for at least 6 months prior to the last sample collected; (iii) no history of systemic antibiotic use in the last 30 days before the sample was collected; (iv) no history of underlying primary immunodeficiency, active malignancy, or systemic corticosteroid use for 2 weeks or more prior to sample collection; and (v) written informed consent from parent or legal guardian. Exclusion criteria for controls: (i) if any member of the household was employed in animal-related occupations; (ii) if the matched control child differed in age from the pet-owning child by more than 12 months; (iii) if the child had been a pet owner during the last year. The age (±12 months) and district (±25 miles) matched controls were matched to the pet-owning enrollees. The matching was done at the time of enrolment, using a sequentially updated matching register.

Sample Size Calculation

Sample size was determined by the two proportions z-test formula in OpenEpi v3.01, an open-access epidemiological calculator (available online at www.openepi.com). The following a priori assumptions were made: Expected pathogen carriage prevalence of 15% in control households (based on three PHCs in the region participated in a pilot study in 2023; n = 40 children) and 40% in pet households (published data from similar settings in Iran and Turkey); the odds ratio was assumed to be 3.7; alpha = 0.05 (two-tailed) and power = 80%. The minimum sample was 78 participants per group. Accounting for an anticipated 15–18% attrition rate (due to incomplete specimen sets, recent antibiotic use, or withdrawal of consent), a recruitment target of 95 children per group (three pet groups + one control group) was set, for a planned total of 380 children (95 per group × 4 groups). There were 412 children screened, of which 378 children had all the eligibility criteria and were included in the final analysis (see Enrollment Flowchart in Supplementary Figure S1).

Specimen Collection

Child Specimens

To control for diurnal variation, all specimens from children were taken at the household during one scheduled home visit between 07:00 and 11:00 h. The collection was done by a trained nurse who had at least two years' clinical experience with pediatrics patients and had attended a standardized training module on specimen collection. For each child, the following four types of specimens were collected:

Fresh stool sample: The parents were asked the previous day to take a single, fresh stool sample in a sterile cryovial (Sarstedt, Germany; 50 ml screw-cap) within 2 hours after defecation. Target volume was 250–500 mg. Samples were picked up and stored immediately at 4°C and processed within 24 hours of collection.

Nasal swab: BD ESwab liquid transport medium (Becton Dickinson, USA) was used to take a swab from each anterior naris and rotated twice. This specimen was used for *Staphylococcus aureus* (including MRSA) and *Pasteurella* nasal colonization.

(c) Skin swab: A second BD ESwab was swabbed after gentle abrasion with a sterile spatula in order to maximize the recovery of superficial dermatophytes and *Staphylococcus* from the antecubital fossa. Visible skin lesions (erythema, scaling, and pustules) were also swabbed and recorded.

Blood specimen: A single 2 mL venous blood sample (within the safe pediatric blood volume guidelines of <3 mL/kg per procedure) was obtained from the antecubital vein under sterile conditions into a serum separator tube (SST; Becton Dickinson) for Toxocara IgG serology. Blood was left to clot for 30 min at room temperature, centrifuged at 1500 × g for 10 min, and stored at −20°C until ELISA. No repeated venipuncture was undertaken; blood was only collected once per child.

Pet Specimens

Pet specimens were collected right after child specimens were collected during the same home visit by a veterinary technician trained in companion-animal sampling. Matched pet specimens were obtained from the main pet in the home:

Dogs and cats: (i) Rectal swab – sterile Copan FecalSwab (Copan Diagnostics, Italy) inserted 2-3 cm and swirled; (ii) Fecal sample (≥1 g) – collected fresh within 4 h from the litter box or defecation site into a cryovial using a sterile spatula; (iii) Fur swab – BD ESwab that is swabbed on the dorsal neck region; (iv) Nasal swab – same as for children. Fecal samples from the cage floor (≥0.5 g fresh fecal material) were collected. Birds were sampled by taking (i) Cloacal swab using a microbiological flocked swab (3 mm diameter) moistened with phosphate-buffered saline (PBS) and inserted 1 cm into the cloaca, (ii) Fecal sample from the cage floor (≥0.5 g fresh fecal material), (iii) Feathers (from breast and dorsal regions), and (iv) Environmental swab (cage feeding tray). All specimens, collected from both children and their matched pets, were labelled with a unique household ID. They were transported within 4 h of collection in an insulated cool box at a temperature of 4°C and delivered to the microbiology laboratory at the College of Science, University of Mosul. Any specimen that arrived at the laboratory after 4 h was excluded from processing; the remaining specimens from the same household were still included in the analysis.

Parasitological Methods

Fecal parasitology was carried out using three complementary methods: (i) direct wet smear in saline and Lugol's iodine (×100 and ×400); (ii) formal-ether concentration technique (Ridley method 1 g stool emulsified in 7 ml 10% formal, filtered through gauze, added 3 ml diethyl ether, centrifuged at 500 × g for 1 min, 4-layer sediment examined at ×100 and ×400); (iii) modified Kinyoun cold acid-fast stain (acid-fast 4–6 µm, carbol fuchsin stain, 3 min, decolorized with 1% sulphuric acid, counterstained with malachite green). To make a specimen negative, at least 50 high-power fields (×400) were examined. Serology for *Toxocara* IgG was carried out on stored serum with a commercially validated ELISA kit (BORDIER Affinity Products, Crissier, Switzerland; Cat. No. is based on secretory-excretory (SE) antigens of second-stage *Toxocara larvae* (No. 9100-0100). The assay was carried out as instructed by the manufacturer: 100 µl of serum was diluted 1:100 in sample diluent and incubated for 30 min at 37°C, followed by a five-fold wash with wash buffer, a 30 min incubation with 100 µl of the HRP-conjugated anti-human IgG, a 15 min incubation with substrate TMB, and stopped with 1N H_2SO_4. Absorbance measured at 450 nm (using 620 nm as a reference wavelength) with a BioTek ELx808 microplate reader. A manufacturer-validated optical density (OD) cut-off of ≥0.200 (OD ratio of ≥1.0 compared to the positive control supplied) was used. Each plate contained positive controls and negative controls in duplicate, and a serum pool of three healthy adult persons known to be negative was used as an in-house negative control. Plates were repeated if the OD values were outside the manufacturer's optimum range.

Molecular Methods

The total DNA was extracted from 200 mg stool or 200 µl swab eluate with the QIAamp DNA Stool Mini Kit (Qiagen, Germany) following the manufacturer's protocol for Pathogen Detection with an additional 5 min incubation time in InhibitEX buffer. The NanoDrop One spectrophotometer (Thermo Fisher Scientific) was used to determine the yield and quality of the DNA, and any samples with an OD260/230<1.50 or an OD260/280<1.70 were re-extracted. The extracted DNA was placed in freezer at -20°C till use. *C. psittaci* detection by real-time PCR: The gene (outer membrane protein A) was targeted using the following primers probe: forward 5'-ATGAAAAAACTCTTGAAATCGG-3', reverse 5'-TTAGAATCTGAATTGAGCATCTTG-3', and probe FAM-TCTACAAGCGCTCCGAAGCTTACC-BHQ1. Reactions (20 µl) included 10 µl TaqMan Fast Universal PCR Master Mix (2×; Applied Biosystems), 900 nM each of the primers, 250 nM of the probe, and 2 µl of the template. Cycling on an Applied Biosystems QuantStudio 3: 95°C 20 s; 45 × (95°C 3 s, 60°C 30 s). Positive control: *C. psittaci* ATCC VR-125 lysate (100 copies/reaction). Extraction blank (nuclease-free water) is run on each plate as negative controls. Positive specimens were defined as those having a Ct of ≤38. *Cryptosporidium* spp. by nested PCR: A nested PCR

targeting the *18S rRNA* gene was used as previously described by Xiao et al. (2000). Outer primers: Cry15 (5'-CCTTGTTACGACTTTTACTTCC-3') and Cry9 (5'-AATACAAATGGCGGTAACAAGGAG-3') giving a ~830 bp product; Inner primers: Cry16 (5'-GGATTTACGATCAGGTCCGTTC-3') and Cry2 (5'-CCTGCTTTAAGCACTCTAATTTTC-3') giving a ~590 bp product. Primary PCR: 95°C 5 min; 35 × (94°C 45 s, 55°C 45 s, 72°C 60 s); 72°C 7 min. Nested PCR: 2 µl primary products as template; identical cycling. Products that were separated on agarose gel (1.5%). Dermatophyte identification: Skin swab eluates were cultured on Sabouraud Dextrose Agar (SDA) with Chloramphenicol 0.05 g/L and *Cycloheximide* 0.4 g/L (Dermasel selective medium; Oxoid) at 28°C for up to 21 days. Growth was measured every 3 days. Macroscopic colonies were identified by color, texture, and morphology, while microscopic colonies were further identified by lactophenol cotton blue wet mount of conidia morphology. All primary isolates were identified using MALDI-TOF, following the same procedure as described above.

Antimicrobial Susceptibility Testing

All confirmed bacterial isolates of *Campylobacter* spp., *Salmonella* spp. and *P. multocida* were subjected to antimicrobial susceptibility testing (AST) by broth microdilution (BMD) minimum inhibitory concentration (MIC) method according to EUCAST standard operating procedure version 9.3.1 (January 2023). Inoculum preparation: Fresh colonies (18–24 hours' growth) were suspended in CAMHB to turbidity 0.5 McFarland (1–2 × 108 CFU/ml) using a DensiCheck instrument (bioMérieux) and the resulting inoculum was diluted 1:100 in CAMHB to obtain a final inoculum of ~5 × 105 CFU/ml per well. *Campylobacter* was cultured on Mueller-Hinton agar with 5% defibrinated horse blood (MH-F; Oxoid) and incubated under microaerophilic conditions at 42°C for 48 h. MIC values were determined at 48 h (*Campylobacter*) or after 18–20 h (*Salmonella*, *Pasteurella*) when the lowest concentration of the antibiotic that does not produce turbidity or pellet was detected under indirect illumination. Reference strains *C. jejuni* ATCC 33560, *S. typhimurium* ATCC 14028 and *P. multocida* ATCC 12945 were used for quality control for each test day. Re-standardization of inoculum preparation was indicated by the results of QC values out of the expected limits on >1 test plate per 20 test plates. The clinical breakpoints tables (EUCAST v13.0, 2023) were used for the breakpoints. Multi-drug resistance (MDR) was considered as resistance against at least an agent from three different classes of antibiotic drugs according to the international consensus definitions (Magiorakos et al., 2012, Clin Microbiol Infect 18:268–281).

Household Survey and Questionnaire

For this study, a structured, interviewer-administered questionnaire was developed de novo and pilot-tested in 15 households in a non-study district (Al-Muthanna) in December 2024, and improvements were made according to the pilot responses. The Arabic instrument was administered by the trained enumerator to the primary caregiver at the time of specimen collection. The questionnaire was structured according to the following domains (summarized in the supplementary files): Household SES: monthly income of the household (ranked by quintile of national income); highest level of education achieved by parents (primary/secondary/college or above); crowding effect (persons per room); source of drinking water (municipal piped water/bottled water/tanker water/wells); type of toilet facility (flush/pit latrine). Pet information: species, breed, age, gender, months since purchase, indoor/outside, child's sleeping position, number of vet visits per year, vaccine type, monthly vaccine visits, and deworming type and yearly deworming visits. Hygiene behaviors: regression handling (never/sometimes/usually/always, converted to a binary always/not-always variable), gloves when handling pet feces, frequency of bathing the pet, and whether ever bitten, scratched, or licked by the pet. All questionnaire data were entered by two independent data entry operators, and discrepancies were resolved by re-inspection of the original paper form, all of which were entered into REDCap (Research Electronic Data Capture, Vanderbilt University), a double data entry, web-

based software system. The percentage of missing values was less than 2% for all variables, and complete-case analysis was used.

Clinical Assessment

The nurse conducted a quick standardized symptom screening of every child in the home with a structured checklist, similar to that used in the WHO Integrated Management of Childhood Illness (IMCI) program at the time of the home visit. The following symptom domains were recorded: gastrointestinal (diarrhea - ≥3 loose stools/day; vomiting; abdominal pain; blood/mucous in stool); respiratory (cough - >2 weeks; dyspnea; chest sounds); dermatological (rash; scaling; erythema; pruritus); constitutional (fever >38°C (axillary); weight loss; fatigue). Children were considered to be symptomatic if the domain was positive and negative if all the domains were negative. No changes were made to specimen processing based on results, and clinical data were obtained without the influence of laboratory results.

Statistical Analysis

Some visualizations were created using the software package IBM SPSS Statistics v28.0 (IBM Corp., Armonk, NY, USA) and the free software package R v4.3.1 (R Foundation for Statistical Computing). Data for continuous variables were presented as mean ± SD or median (IQR) depending on the distribution of the data and the result of the Shapiro-Wilk test. Frequency (n) and percentage (%) were used to represent categorical variables.

The Pearson chi-square test (or Fisher's exact test if any cell count was <5) was used to determine differences in prevalence proportions between groups. Any detection of a zoonotic pathogen was considered as a binary outcome (1 = at least one pathogen detected; 0 = no pathogen detected) for binary logistic regression. All variables having univariate p-value < 0.20 were included in the multivariable model. A backward stepwise elimination procedure with a p-value of >0.10 for the removal of variables was used. The Hosmer-Lemeshow goodness of fit test for the model was used ($p > 0.05$ accepted). Odds ratio (cOR and aOR) with 95% confidence intervals (CI) are reported. The statistical significance was considered as a two-tailed p-value < 0.05 for all the tests. Seasonal analysis: calendar months were combined into four weather seasons, suitable for this semi-arid climate: (March-May), (June-August), (September-November) and (December-February). The frequencies of occurrence of pathogens were compared by season based on a chi-square test. For comparisons of the antimicrobial resistance rates between isolates of children and matched pet isolates, McNemar's test for paired proportions was used. All the statistical tests used for each outcome measure are summarized in Table M7.

Quality Assurance

Repeat administration by the second enumerator (blinded to the first result) within 48 h was conducted in 10% of the households (n = 38) to assess the inter-rater reliability for the administration of the questionnaire; the kappa was ≥0.81 for all the key variables. The clinical and questionnaire data were kept from the laboratory personnel while processing the specimens. All culture media were tested for quality on the day of preparation with the appropriate ATCC reference strains. The equipment calibration (incubator, centrifuge, spectrophotometer and microplate reader) was recorded weekly. External quality control for identification of MALDI-TOF was ensured by taking part in UK NEQAS (National External Quality Assessment Service) for microbial identification (quarterly panels).

Results

Enrollment and Demographic Characteristics

A total of 412 children were screened between January and December 2025; 378 were eligible and enrolled (dog group n = 124; cat n = 98; bird n = 67; control n = 89). Thirty-four were not included (incomplete specimen's n = 18, recent antibiotics n = 11, incomplete consent n = 5). There were no statistically significant

differences in age or sex between groups (Table 1). Mean age was 7.4 ± 2.1 years; 53.4% were male. In terms of pet characteristics, 79.0% of dogs were vaccinated against core diseases as compared to 53.1% of cats. Birds were only kept indoors. The median dog, cat, and bird pet ownership time was 28.3, 22.7, and 18.4 months, respectively.

Table 1. Demographic and Household Characteristics of Study Participants

Characteristic	Group A (Dogs) n=124	Group B (Cats) n=98	Group C (Birds) n=67	Control (No Pet) n=89
Age (years), Mean±SD	7.2±2.1	7.5±1.9	7.8±2.3	7.1±2.0
Male, n (%)	68 (54.8)	52 (53.1)	35 (52.2)	46 (51.7)
Female, n (%)	56 (45.2)	46 (46.9)	32 (47.8)	43 (48.3)
Urban residence, n (%)	89 (71.8)	74 (75.5)	48 (71.6)	66 (74.2)
Rural residence, n (%)	35 (28.2)	24 (24.5)	19 (28.4)	23 (25.8)
Low SES, n (%)	42 (33.9)	29 (29.6)	23 (34.3)	28 (31.5)
Duration of pet ownership (months)	28.3±14.6	22.7±12.8	18.4±10.2	N/A
Indoor-only pet, n (%)	61 (49.2)	71 (72.4)	67 (100)	N/A
Vaccinated pet, n (%)	98 (79.0)	52 (53.1)	N/A	N/A

SES: Socioeconomic status; N/A: Not applicable.

Overall Zoonotic Pathogen Detection Rates

At least one specimen of 180 of 378 children (47.6% overall) tested positive for at least one zoonotic pathogen. Stratified rates were: dog-owning 48.4% (60/124), cat-owning 52.0% (51/98), bird-owning 38.8% (26/67), and control 14.6% (13/89), all p<0.001 vs. control, Table 2.

Specific Pathogen Findings

Toxocara spp.

Toxocara seropositivity was detected in 22.4% of cat-owning (22/98) and 18.5% of dog-owning children (23/124), versus 3.4% of controls (3/89) (*p=0.001*). There was no presence of toxocara in the children who kept birds, as would be expected. Seropositive children were younger (5.8+/-1.7 vs. 8.1+/-2.0 years, *p<0.001*), more likely to live in low-SES families (68.4%), and more likely to have a pet indoors (73.7%).

Campylobacter spp.

Campylobacter was the most prevalent bacterial pathogen on the whole, with 46 children (12.2%). It was predominant among cat-owning (16.3%), dog-owning (14.5%), bird-owning (8.9%), and control households (4.5%). All isolates were *C. jejuni* (71.7%) or C. coli (28.3%) by MALDI-TOF. The same *Campylobacter* strains were identified in matching pets in 78.3% of culture-positive households, which is a strong argument in favor of intra-household transmission.

Table 2. Prevalence of Specific Zoonotic Pathogens by Household Pet Type

Pathogen	Group A Dogs (%)	Group B Cats (%)	Group C Birds (%)	Control (%)	*p-value*
Toxocara canis/cati	18.5	22.4	0	3.4	*0.001*
Campylobacter spp.	14.5	16.3	8.9	4.5	*0.003*
Salmonella spp.	8.1	12.2	23.9	3.4	*<0.001*
Pasteurella multocida	9.7	18.4	0	0	*<0.001*
S. aureus (MRSA)	6.5	5.1	4.5	2.2	*0.14*
Chlamydia psittaci	0	0	11.9	0	*<0.001*
Cryptosporidium spp.	4.0	6.1	3.0	1.1	*0.04*
Dermatophytes	7.3	15.3	0	2.2	*0.002*
Any pathogen detected	48.4	52.0	38.8	14.6	*<0.001*

Percentages indicate proportion of children in each group with confirmed pathogen detection. p-values from chi-square test.

Salmonella spp.

Salmonella was detected in 39 children (10.3%), with the highest prevalence in bird-owning households (23.9%), followed by cats (12.2%), dogs (8.1%), and controls (3.4%) (*p<0.001*). *S.* Typhimurium (43.6%), *S. Enteritidis* (33.3%), and *S. stanley* (12.8%) were the most common serotypes. Interestingly, 23.9 percent of *Salmonella*-positive bird households had just purchased birds at open-air markets without veterinary inspection.

Chlamydia psittaci

The *C. psittaci* was only identified in the bird-owning group (11.9 %, 8/67). All positive cases were confirmed by real-time PCR (ompA). Eight positive children (75% of those who were positive) were exposed to newly acquired birds in the last 6 months. In 87.5% cases (dry cough, fever, atypical pneumonia) there were clinical manifestations, and 3 children (37.5 %) were hospitalized - the highest hospitalization rate among all groups of pathogens.

Pasteurella multocida

Pasteurella multocida was detected in 18.4 percent of cat-owning children (18/98) and 9.7 percent of dog-owning children (12/124), but none of the bird- or control children (*p<0.001*). A history of a bite, scratch, or frequent close oral contact with their pet was documented in all positive children.

Risk Factor Analysis

The use of multivariate logistic regression revealed nine independent risk factors that were significantly related to the acquisition of zoonotic pathogens (Table 3). The strongest predictor was owning an unvaccinated pet (adjusted OR = 4.19, 95% CI: 2.33–8.35, *p<0.001*), followed by child age <5 years (aOR = 3.65, 95% CI: 2.10–6.81, *p<0.001*), and absence of handwashing after pet contact (aOR = 3.07, 95% CI: 1.78–5.75, *p<0.001*). Cat ownership conferred a higher risk (aOR = 2.98) than dog (aOR = 2.54) or bird ownership (aOR = 2.05).

Table 3. Multivariate Logistic Regression: Independent Risk Factors for Zoonotic Pathogen Acquisition

Risk Factor	Crude OR	95% CI	*p-value*	Adjusted OR
Cat ownership	3.12	1.84–5.29	*<0.001*	2.98

Dog ownership	2.67	1.56–4.57	*0.001*	2.54
Bird ownership	2.18	1.22–3.90	*0.009*	2.05
Unvaccinated pet	4.41	2.33–8.35	*<0.001*	4.19
Child age < 5 years	3.78	2.10–6.81	*<0.001*	3.65
Low socioeconomic status	2.25	1.31–3.86	*0.003*	2.11
Rural residence	1.89	1.04–3.44	*0.037*	1.74
Outdoor pet access	2.54	1.41–4.57	*0.002*	2.38
No handwashing after pet contact	3.20	1.78–5.75	*<0.001*	3.07

OR: Odds Ratio; CI: Confidence Interval. All variables adjusted for each other in the final model.

Clinical Manifestations

In 180 pathogen-positive children, 35.0% -38.5% were asymptomatic on the day of specimen collection across groups of pets, as opposed to 69.2% in the control positives. The highest prevalence of *Chlamydia psittaci* and *Salmonella* was reflected in the occurrence of gastrointestinal symptoms in the dog and cat groups, and respiratory symptoms in the bird group. Dermatological presentation was found in 20.0% of dog-group positive children and 31.4% of cat-group positive children, respectively, consistent with the dermatophyte and *Pasteurella* carriage rates observed in these groups.

Antimicrobial Resistance

Among 168 bacterial isolates tested, high resistance rates were detected for all three genera. *Campylobacter* showed the highest MDR rate (22.6%), with particularly elevated tetracycline (52.6%) and ciprofloxacin (38.7%) resistance. *Salmonella* showed 38.6% ampicillin and 18.2% MDR. Resistance profiles of child-derived isolates closely matched those of corresponding pet isolates, suggesting a shared within-household resistance gene pool. For *P. multocida*, overall antibiotic resistance to beta-lactams was low; however, 16% of isolates exhibited decreased tetracycline susceptibility.

Co-infection with two or more pathogens simultaneously was observed in 17 children (9.4% of all positives). Co-infection patterns varied by pet group; the dog group most commonly showed *Toxocara/Campylobacter* co-infection, the cat group *Toxocara/Pasteurella* or *Toxocara/Dermatophyte*, and the bird group *Salmonella/Campylobacter*. These co-infection patterns are summarized in Figure 1.

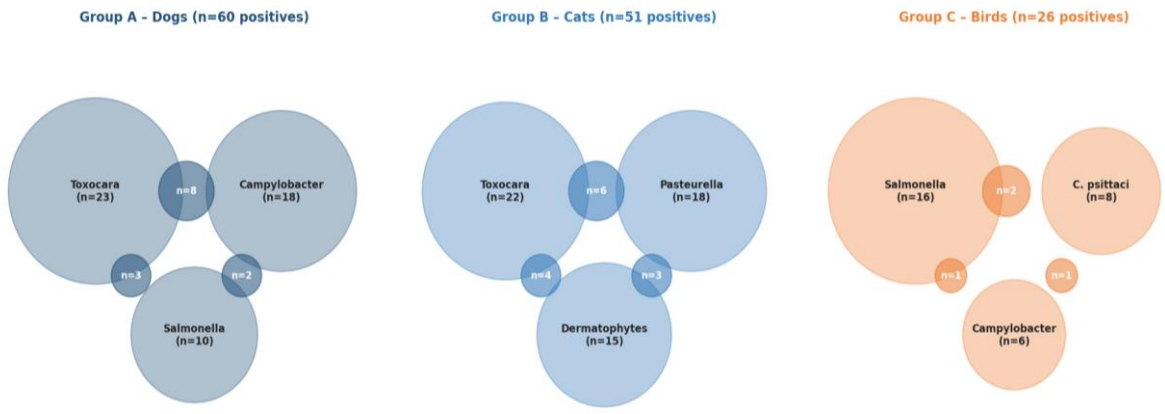

Fig. 1. Co-infection patterns among pathogen-positive children stratified by pet ownership group. Bubble size is proportional to the number of single-pathogen cases. Overlapping regions indicate dual-pathogen co-detection, with absolute numbers of co-infected children shown in white.

Discussion

To the best of our knowledge, this is the first study to present comprehensive multi-pathogen epidemiological data on pet-to-child zoonotic transmission in Iraq. We found significantly higher rates of zoonotic pathogen carriage in children who lived with pets than controls, with detection rates of 38.8%-52.0% of the three pets versus 14.6% in the control group ($p<0.001$ in all comparisons). This burden, as visualized in all eight pathogens tested in Figure 2, does not belong to any one organism but represents a general risk, covering a wide spectrum of intimate human-pet contact.

The overall prevalence (47.6) is significantly higher than those reported in European studies (15–25%) and is similar to those obtained in Egypt (42.3%), Iran (38.7%), and Turkey (44.8%) (19-21). This increased prevalence in low-income environments is probably a combination of reduced pet vaccination rates, reduced access to veterinary care, increased outdoor pet access, and poorer hygiene which were all found to be independent risk factors in our multivariate model.

The results of identifying unvaccinated pets as the most powerful independent risk factor (aOR = 4.19) are critically actionable. In Iraq, pet vaccination is not legally mandated, with the exception of rabies vaccination for dogs. The fact that only 79% of the enrolled dogs and 53.1% of cats were vaccinated - in households that presented to veterinary clinics, which is likely an overestimation of population-level estimates - highlights that unvaccinated pets are the one most modifiable risk in this case (22, 23).

Children below the age of five have an age vulnerability of 3.65, which conforms to the well-known immunological and behavioral vulnerability of this age group. Immunological immaturity in response to enteric pathogens, contact with the mouth, and increased close physical contact with pets increase the risk of exposure (24, 25). This result immensely endorses specific counseling for families that own pets and have children of this age group.

The fact that *Chlamydia psittaci* was only found in the group with birds (11.9%), is very clinically significant. Psittacosis may manifest as typical severe and atypical pneumonia and is often confused with community-acquired bacterial pneumonia (26, 27). The severity of *C. psittaci* infection is supported by our observation that 87.5% of children with *C. psittaci*-positive results had respiratory symptoms and 37.5% of them needed hospitalization, which is the highest hospitalization rate of all the pathogen groups. Amazingly, there is no established surveillance of *C. psittaci* in Iraq, and the pathogen is not part of the routine algorithms of differential diagnosis of pediatric pneumonia, which generates probable underdiagnoses.

A very worrying aspect is the antimicrobial resistance data. The *Campylobacter* and Salmonella rates of 22.6 and 18.2% are significantly higher than the European surveillance rates (6 to 10% and 8 to 12% respectively) and are comparable to the rates in Iran and Turkey (28, 29). The occurrence of *Campylobacter* resistance to fluoroquinolone (38.7% ciprofloxacin resistant) is particularly alarming since ciprofloxacin is widely employed as first-line empirical treatment of pediatric enteric infections in Iraqi clinical practice (30). The highly similar patterns of resistance observed in the pet and child isolates in the same households are strong arguments in support of intra-household infection of resistant strains (31, 32).

The high summer transmission (39.3% of total cases during the study period) can be attributed to the thermophilic survival ability of Campylobacter and Salmonella, high outdoor activities in hot climates in Iraq, and behavioral patterns such as water play and consuming raw foods during the summer period (33-35). Such seasonal peaks offer valuable periods for targeting public health campaigns.

The co-infection statistics indicate that a significant percentage of pathogen-positive children (9.4%) have two pathogens co-infecting them, and the distributions vary across pet types. This has clinical implications: when a child with cats presents with gastrointestinal and dermatological symptoms, *Pasteurella*, *Toxocara*, and dermatophyte co-infections should be considered together as a syndromic cluster, not evaluated as sequential, independent diagnoses (36, 37).

Limitations of the study are that the cross-sectional design does not allow causal inference, single-city sampling does not allow generalization, and whole-genome sequencing was not done to determine clonal transmission events, but MALDI-TOF and resistance profile matching were done. These strengths are prospective design, systematic dual (child + pet) specimen collection, validated laboratory procedures, a robust multivariate analysis, and a comprehensive panel of pathogens (18, 38).

Our results highly recommend a One Health approach to zoonotic surveillance in Iraq. Recommendations based on evidence involve: compulsory vaccination and deworming of pets; regular veterinary screening of marketplace pets; *C. psittaci* should be included in diagnostic panels of pediatric pneumonia in households with birds; specific hygiene education initiatives; and antimicrobial susceptibility monitoring should become part of national AMR surveillance (7,28,29,31,32,39).

Conclusion

This cross-sectional study is the first of its kind to show that the presence of pets in households in Mosul, Iraq, is linked to a greatly increased risk of carrying zoonotic pathogens in childhood, with a higher rate of detection compared to household with controls, 2.7-3.6 times. The zoonotic risk profile of cats, dogs, and birds is different: cats have the greatest overall burden (52.0%), birds are unique transmitters of *Chlamydia psittaci* with the highest hospitalization rate, and all types of pets have an enteric pathogen burden. The extensive rates of antimicrobial resistance, such as fluoroquinolone resistance in *Campylobacter* and multi-drug resistance in *Salmonella*, in household transmission chains are a pressing antimicrobial stewardship issue.

Modifiable risk factors such as pet vaccination, age of children, handwashing, and socioeconomic conditions have clear and actionable targets to improve the health of the population. The findings form a powerful argument to justify the creation of national guidelines on the prevention of pet zoonosis and integrated One Health surveillance programs in Iraq. The proposed study should be followed by longitudinal cohort studies, whole-genome sequencing to verify the transmission cases, and cost-effectiveness investigations of the suggested interventions.

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Conflict of Interest

The author reports that there were no conflicts of interest.

Ethical approval

The study protocol has been approved by the Scientific Committee of the College of Science, University of Mosul. Since all samples were collected simply for observation and diagnostic purposes, no clinical intervention and experimental manipulation was done. Informed consent, written for the parent/legal guardian of all child participants, and verbal assent from children ≥7 years was obtained before enrolment. It was explained to the participants that they have the freedom to stop at any time without repercussions.

Artificial Intelligence Statement

AI tools were only used for language editing and formatting support in the process of manuscript preparation. The study design, data collection, statistical analysis, and interpretation of results were not conducted by an AI system. The author is solely responsible for the scientific content, methodology, and conclusions.

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