

Preplanned Studies

Metagenomic Next-Generation Sequencing Analysis of Pathogens in Infected Wounds from Dog and Cat Bites — China, 2021–2025

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Summary

What is already known about this topic?

Dog and cat bites frequently develop polymicrobial wound infections requiring prompt and appropriate antimicrobial treatment. However, conventional culture-based methods often fail to identify all pathogens, particularly anaerobic and fastidious microorganisms.

What is added by this report?

This study used metagenomic next-generation sequencing (mNGS) to analyze infected dog- and cat-bite wounds. Distinct microbial profiles were identified between dog and cat bites, and between domestic and stray animals. Anaerobes were predominant in both groups.

What are the implications for public health practice?

These findings highlight the value of mNGS and support empirical antimicrobial strategies to improve infection management and reduce complications.

In total, 178 bacterial species were identified. At the genus level, *Streptococcus*, *Pasteurella*, and *Porphyromonas* were predominant in dog bite samples, whereas *Pasteurella*, *Fusobacterium*, and *Bacteroides* were predominant in cat bite samples. Anaerobes outnumbered aerobes in both groups, with a significantly higher ratio in dog bites than in cat bites (2:1 *vs.* 1.6:1, $P=0.007$). Stray animals were associated with more diverse pathogen profiles than domestic pets.

Conclusion: Dog- and cat-bite wounds harbor distinct, anaerobe-predominant polymicrobial communities. mNGS enables comprehensive pathogen identification beyond the capacity of conventional culture methods and may support optimized empirical antimicrobial therapy, particularly routine anaerobic coverage tailored to the animal type and domestication status.

ABSTRACT

Introduction: Dog and cat bites frequently cause complex wound infections. However, traditional pathogen detection methods often fail to fully characterize the microbial spectrum involved, hindering effective antimicrobial therapy.

Methods: This retrospective study enrolled 77 patients with infected dog- or cat-bite wounds admitted to the Aerospace Center Hospital, Beijing, China, between October 2021 and April 2025. Wound specimens were analyzed using metagenomic next-generation sequencing (mNGS) on an MGISEQ-200 platform, with bioinformatics analysis performed using Pathogenic Microorganism sequencing (PMseq).

Results: The mNGS positivity rates were 94.44% (51/54) for dog bites and 86.96% (20/23) for cat bites.

Dogs and cats are among the most common causes of animal-related traumatic injuries in humans and account for approximately 90% of all animal wounds. Infection develops in approximately 3%–18% of dog-bite wounds and 28%–80% of cat-bite wounds, occasionally leading to severe complications, such as meningitis, infective endocarditis, septic arthritis, and septic shock (1–7). Owing to the complexity of infections and limitations of traditional pathogen detection methods, these injuries continue to pose important public health challenges. In the present study, metagenomic next-generation sequencing (mNGS) was used to analyze infected dog- and cat-bite wounds in 77 patients treated in China between 2021 and 2025. Distinct microbial profiles were identified between dog- and cat-bite infections as well as between domestic and stray animals. The predominant pathogens were *Streptococcus minor*, *Capnocytophaga*

cynodegmi, *Pasteurella* spp. and multiple anaerobic bacteria. Anaerobic bacteria were predominant in both dog- and cat-bite infections, and the anaerobe-to-aerobe ratio was significantly higher in dog bites than in cat bites. These findings highlight the importance of appropriate empirical antimicrobial therapy with routine anaerobic coverage and further demonstrate the value of mNGS for comprehensive pathogen identification in complex bite-wound infections.

This retrospective study recruited patients with infected dog- and cat-bite wounds admitted to the emergency department of the Aerospace Center Hospital (Beijing, China) between October 2021 and April 2025. Patients were included if they presented with at least one of the following: local erythema, swelling, or pain at the wound site; fever (≥ 38.0 °C) without another apparent cause; abscess formation; or lymphangitis. Data on patient age, sex, bite-related characteristics, infectious manifestations, treatment, and empirical antibiotic exposure before mNGS were collected and included in the analysis. Medical records were reviewed, and telephone follow-up was conducted until infection-related symptoms were resolved.

For specimen collection, needle aspiration was performed for abscesses, standard cotton swabs for open lacerations, and treated cotton swabs for puncture wounds. The specimens were subjected to nucleic acid extraction, pathogen enrichment, nucleic acid fragmentation, library preparation, and sequencing on an MGISEQ-200 platform using the corresponding

sequencing kit (MGI, China).

Bioinformatics analysis was conducted using PMseq Raw FASTQ sequencing data that underwent quality control and evaluation using Trimmomatic (version 0.40; Forschungszentrum Jülich, Jülich, Germany). During this step, low-quality or undetected reads, adapter-contaminated sequences, high-coverage repetitive elements, and excessively short fragments were filtered to retain high-quality data. Subsequently, the cleaned sequences were aligned against the human reference genome GRCh37 (hg19) using Bowtie2 (version 2.4.3; Johns Hopkins University, Baltimore, Maryland, USA), yielding pathogen-free datasets for downstream analyses. Finally, species-level annotation of the clean reads was performed by aligning them with the NCBI GenBank/RefSeq/nt databases using Kraken2 (version 2.1.0; Johns Hopkins University, Baltimore, Maryland, USA), thereby generating definitive microbial identification results.

All statistical analyses were performed using SPSS (version 25.0; IBM Corp., Armonk, NY, USA). Categorical variables were compared using the chi-square test or Fisher's exact test, as appropriate, including comparisons of anaerobe-to-aerobe distributions between dog- and cat-bite samples. Statistical significance was defined as a two-sided $P < 0.05$.

A total of 77 patients with infected bite wounds were ultimately included, comprising 54 dog-bite cases (35 domestic and 19 stray) and 23 cat-bite cases (17

TABLE 1. Basic information of patients with dog- and cat-bite wounds in this study, 2021–2025.

Characteristics	Dog-bite cases (n=54)	Cat-bite cases (n=23)	P
Age, mean±SD (years)	45.51±24.92	51.44±14.68	0.200
Sex, male, n (%)	27 (50.00)	7 (30.43)	0.110
Bite location, n (%)			
Hand	23 (42.59)	15 (65.22)	0.069
Head and face	15 (27.78)	0	0.004
Trunk	12 (22.22)	0	0.014
Upper arm	10 (18.52)	2 (8.70)	0.457
Leg	7 (12.96)	4 (17.39)	0.879
Foot	2 (3.70)	2 (8.70)	0.732
Symptoms, n (%)			
Redness and swelling	24 (44.44)	17 (73.91)	0.018
Purulent exudation	14 (25.93)	4 (17.39)	0.418
Abscess	6 (11.11)	2 (8.70)	1.000
None	10 (18.52)	0	0.028

Abbreviation: SD=standard deviation.

domestic and six stray). Patients' ages ranged from 1 to 83 years, with a mean age of 47 years (Table 1). There were 34 males and 43 females, with no significant differences in age or sex distribution between the dog- and cat-bite groups. The bite locations varied, with the hands (38 patients), head and face (15 patients), trunk (12 patients), and upper arms (12 patients) being the most commonly affected. Head, face, and trunk injuries occurred exclusively in dog bites. Redness and swelling were the most common clinical manifestations and were significantly more frequent in cat-bite cases than in dog-bite cases [17 (73.91%) vs. 24 (44.44%), $P=0.018$; Table 1].

Samples were collected for mNGS analysis based on the infection status of each patient. Most patients received empirical antibiotic treatment before the mNGS sampling. Despite prior antibiotic exposure, major pathogenic microorganisms associated with persistent wound infections could still be detected using mNGS, and no obvious reduction in the overall pathogen positivity was observed. The interval from injury to sampling ranged from 1 to 90 days, with mean intervals of 9.70 ± 16.48 days for dog bites and 7.39 ± 4.66 days for cat bites, without significant differences between groups ($P=0.511$; Figure 1A). Exploratory analysis showed that six cases (7.79%, 6/77) were sampled 15–23 days after injury and three cases (3.90%, 3/77) were sampled more than 60 days after injury. The pathogens identified in these delayed samples remained within the microbial spectrum detected in the samples collected within 14 d after

injury, without the obvious emergence of distinct pathogen patterns. No significant association was observed between sampling interval and pathogen positivity or microbial diversity.

The mNGS positivity rates were 94.44% (51/54) for dog-bite wounds and 86.96% (20/23) for cat-bite wounds, with no significant differences between the groups ($P=0.356$; Figure 1B). Six samples yielded negative results, all of which originated from domestic animals (three dog bites and three cat bites). Among these six cases, four involved hand wounds and two involved lower limb wounds. Five patients presented with redness, swelling, and exudation, whereas one exhibited purulent exudation alone.

At the genus level, 88 bacterial genera were detected in the dog-bite samples, including 37 genera identified in more than 5% of the cases ($n > 2$). The most frequently detected genera were *Streptococcus* ($n=30$), *Pasteurella* ($n=20$), *Porphyromonas* ($n=20$), *Staphylococcus* ($n=20$), *Capnocytophaga* ($n=18$) and *Fusobacterium* ($n=18$). Stratified analysis demonstrated that *Streptococcus* (51.43%), *Pasteurella* (37.14%), and *Fusobacterium* (37.14%) were predominant in domestic dog-bite wounds, whereas *Streptococcus* (63.16%), *Staphylococcus* (57.89%), *Porphyromonas* (42.11%), and *Acinetobacter* (42.11%) were more common (Figure 2A).

In cat-bite wounds, 43 bacterial genera were detected, including 23 genera identified in more than 5% of the cases ($n > 1$). The most frequently detected genera were *Pasteurella* ($n=14$), *Fusobacterium* ($n=12$),

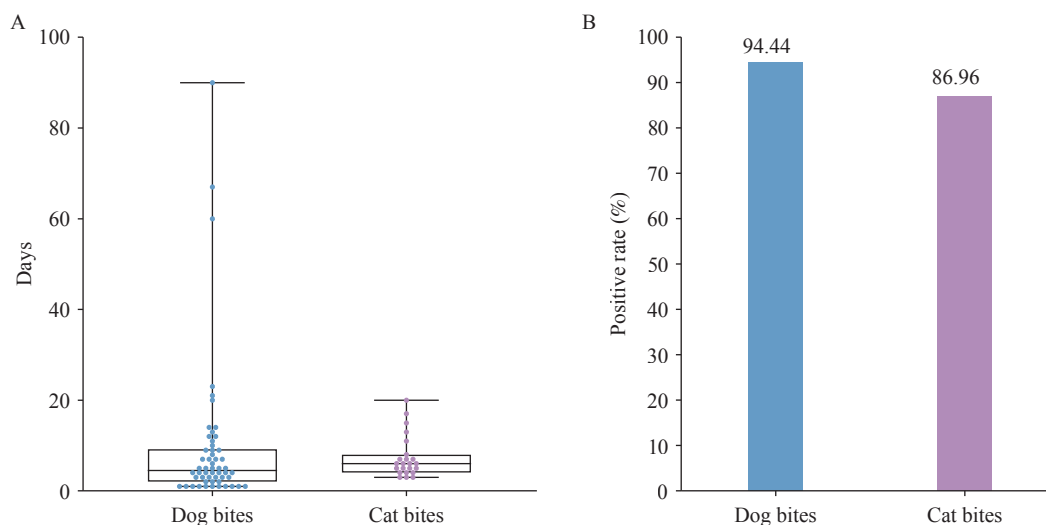


FIGURE 1. Timing of mNGS sampling and pathogen detection positivity. (A) Distribution of the interval between injury and mNGS sampling in dog- and cat-bite patients. (B) Positivity rates of mNGS pathogen detection in dog- and cat-bite wound specimens.

Abbreviation: mNGS=metagenomic next-generation sequencing.

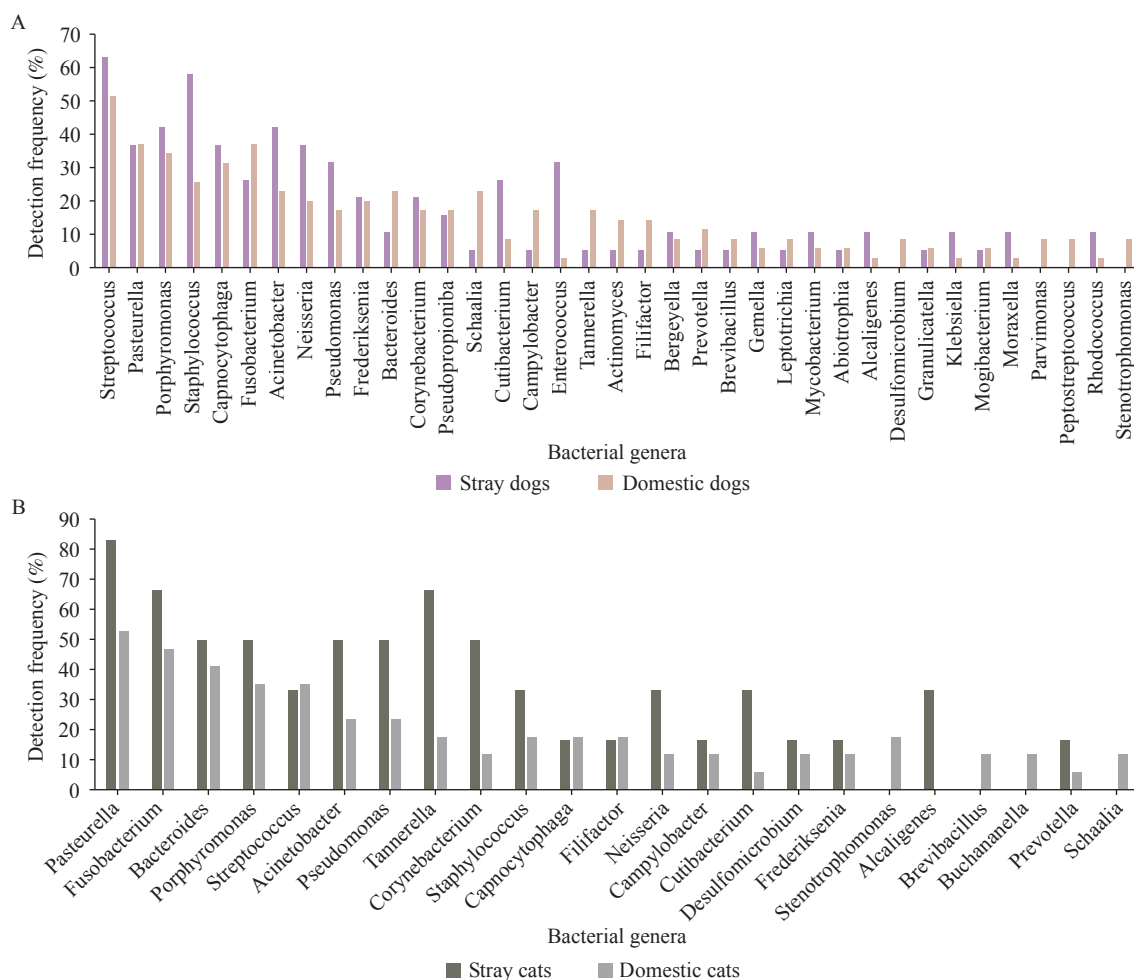


FIGURE 2. Genus-level bacterial profiles in infected bite-wound specimens. (A) Dog-bite wounds stratified by domestic versus stray dogs; (B) Cat-bite wounds stratified by domestic versus stray cats.

Note: Only genera detected at a frequency >5% were included in the figure.

Bacteroides ($n=10$), *Porphyromonas* ($n=9$) and *Streptococcus* ($n=8$). Domestic cat-bite wounds were mainly characterized by *Pasteurella* (52.94%), *Fusobacterium* (47.06%), and *Bacteroides* (41.18%), whereas stray cat-bite wounds showed particularly high detection rates for *Pasteurella* (83.33%), *Fusobacterium* (66.67%), and *Tannerella* (66.67%) (Figure 2B).

Fungi and viruses were rarely detected. Fungi detected mainly included *Aspergillus*, *Candida*, and *Malassezia* species. Viral detection was uncommon and mainly involved low-abundance sequence signals of uncertain clinical significance. The detailed distributions of the fungal pathogens are provided in Supplementary Table S1 (available at <https://weekly.chinacdc.cn/>).

In total, 178 bacterial species were identified. Among these, 108 species were detected in the dog-bite wounds, 19 were exclusive to the cat-bite wounds, and

51 were shared between the two groups. Anaerobic bacteria outnumbered aerobic bacteria in both dog- and cat-bite infections. The anaerobe-to-aerobe ratio was 2:1 for dog bites and 1.6:1 for cat bites, with a statistically significant difference between the groups (Pearson's chi-square test, $P=0.006$; Fisher's exact test, $P=0.007$). Among anaerobic bacteria, the most common Gram-positive species in dog-bite wounds were *Pseudopropionibacterium propionicum*, *Cutibacterium acnes*, and *Schaalia canis*, whereas the predominant Gram-negative anaerobes were *Porphyromonas cangingivalis*, *Fusobacterium canifelinum*, and *Tannerella forsythia*. In cat-bite wounds, the most common Gram-positive anaerobes were *Filifactor alocis* and *Corynebacterium striatum*, whereas the predominant Gram-negative anaerobes were *Fusobacterium russii*, *Tannerella forsythia*, and *Bacteroides pyogenes*. Among the aerobic bacteria, the

most common gram-positive species in dog-bite wounds were *Streptococcus minor*, *Staphylococcus aureus*, and *Acinetobacter baumannii*, whereas the predominant gram-negative aerobes were *Pasteurella canis*, *Capnocytophaga cynodegmi*, and *Frederiksenia canicola*. In cat-bite wounds, the most common gram-positive aerobic species were *Streptococcus minor*, *Staphylococcus epidermidis*, and *Acinetobacter baumannii*, whereas the predominant gram-negative aerobes were *Pasteurella multocida*, *Alcaligenes faecalis*, and *Pseudomonas stutzeri*

(Figure 3).

Fungal pathogens have rarely been identified. *Candida parapsilosis* and *Aspergillus sydowii* were detected in two stray dog bite wounds. *Malassezia restricta* was detected in two stray dog-bite wounds, *Malassezia japonica* in one stray dog-bite wound, and *Malassezia japonica* and *Malassezia globosa* in one domestic dog-bite wound. *Candida parapsilosis* and *Pichia guilliermondii* were co-present in one domestic cat-bite wound, whereas *Malassezia restricta* was

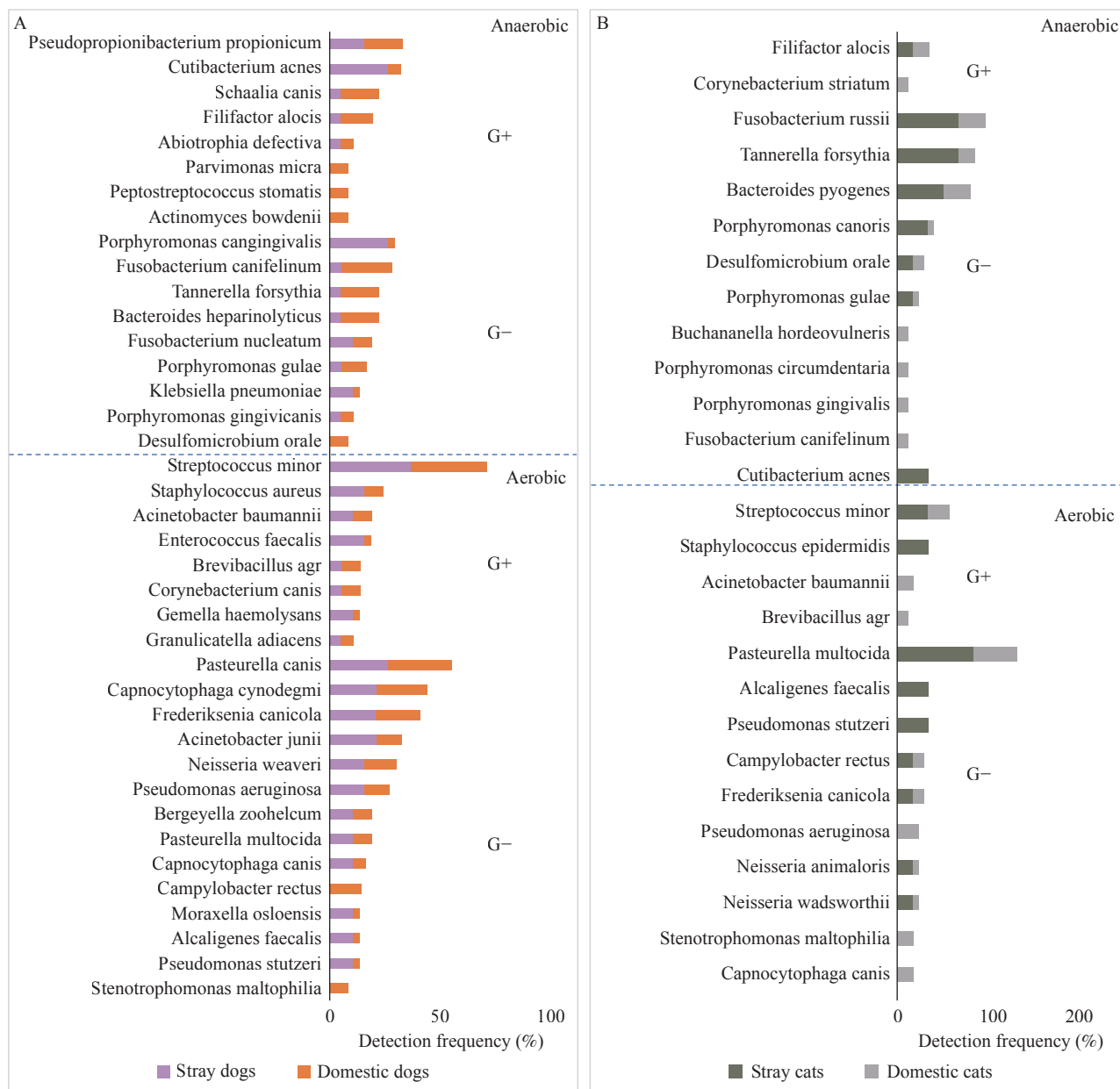


FIGURE 3. Distribution of bacterial taxa identified at the species level in infected bite-wound specimens. (A) Distribution of bacterial species identified in dog-bite wound specimens; (B) Distribution of bacterial species identified in cat-bite wound specimens.

Note: Only bacterial species detected at a frequency >5% in either dog- or cat-bite patients were included in this figure.

identified in two stray cat-bite wounds.

DISCUSSION

Animal bites are among the most common traumatic injuries in humans, and frequently lead to polymicrobial wound infections. In this study, we comprehensively characterized the microbiota of infected dog and cat-bite wounds from 77 Chinese patients using mNGS. Our findings demonstrated distinct microbial profiles according to the animal type (dog *vs.* cat) and domestication status (domestic *vs.* stray). In addition to confirming previously recognized pathogens, mNGS identified a broad spectrum of anaerobic and opportunistic microorganisms that are often difficult to detect using conventional culture-based methods.

Consistent with previous epidemiological studies on bite wound infections (8–9), the hand was the most frequently affected anatomical site in dog and cat-bite injuries. All bites involving the head, face, and trunk were caused by dogs, likely reflecting differences in animal size and attack behavior (10). Redness and swelling were the most common clinical manifestations and were significantly more frequent in cat-bite patients, possibly because cat bites tend to produce deeper puncture wounds with poorer drainage (10–11). The high positivity rates of mNGS in both groups further supported the utility and analytical sensitivity of mNGS for the detection of fastidious and unculturable pathogens in infected wounds (12). In addition, exploratory analysis demonstrated no significant association between the sampling interval and overall pathogen positivity or microbial diversity, suggesting the relative stability of the core pathogenic spectrum across different stages of wound infection.

At the genus level, dog and cat-bite wounds showed distinct distributions of pathogens. *Streptococcus*, *Pasteurella*, and *Porphyromonas* were predominant in dog-bite wounds, whereas *Pasteurella*, *Fusobacterium*, and *Bacteroides* were the most common in cat-bite wounds. These findings are consistent with previous reports that identified *Pasteurella* species and anaerobic bacteria as the major pathogens in animal bite infections (13–14). Stratified analysis further demonstrated the microbial differences between domestic and stray animals. Stray dog bites showed relatively high abundances of *Staphylococcus* and *Acinetobacter*, whereas stray cat bites showed high detection rates of *Pasteurella* and *Tannerella*, suggesting broader environmental microbial exposure

in stray animals (15).

A major finding of this study was the predominance of anaerobic bacteria in both dog and cat bite infections. The anaerobe-to-aerobe ratio was significantly higher in dog-bite wounds than in cat-bite wounds (2:1 *vs.* 1.6:1, Fisher's exact test, $P=0.007$), further supporting the important contribution of anaerobic bacteria to animal bite-wound infections (16–17). These findings highlight the importance of routine anaerobic antimicrobial coverage in empirical treatment regimens for infected bites.

Fungi were rarely detected in the analyzed specimens and mainly included *Candida*, *Aspergillus*, and *Malassezia* spp. Viral detection was also uncommon, and primarily consisted of low-abundance sequence signals of uncertain clinical significance. As RNA sequencing was not included in the current mNGS workflow, RNA viral pathogens could not be comprehensively assessed. Overall, these findings suggest that bacterial pathogens, particularly anaerobic bacteria, are the predominant infectious agents in dog- and cat-bite wounds.

Several microorganisms identified in this study, including anaerobic bacteria, opportunistic pathogens, and environment-associated bacteria detected during stray animal bites, may have important implications for empirical antimicrobial selection. The relatively high abundance of anaerobic bacteria supports the routine inclusion of anaerobic coverage in the empirical treatment strategies for infected bites. In addition, opportunistic pathogens such as *Acinetobacter* and *Staphylococcus* species identified in stray animal bites may reflect broader environmental microbial exposure and could potentially be associated with an increased risk of antimicrobial resistance. Although antimicrobial susceptibility testing was not performed in the current study, these findings provide useful microbiological information for optimizing empirical antibiotic strategies for complex bite-wound infections.

Beyond their implications in antimicrobial selection, the pathogen profiles identified in this study have important clinical and public health implications. The predominance of anaerobic bacteria and frequent detection of polymicrobial infections highlight the limitations of conventional culture-based diagnostic approaches and support the use of advanced molecular diagnostics in complicated or persistent bite wound infections. Furthermore, the distinct microbial profiles observed between dog and cat bites as well as between domestic and stray animals suggest that infection risk assessment and empirical management strategies may

need to be tailored according to the animal source and exposure setting. From a public health perspective, the broader spectrum of opportunistic and environmentally associated pathogens detected in stray animal bites underscores the importance of stray animal management, animal bite surveillance, public education, timely wound care, and early medical intervention. These findings provide epidemiological evidence that may contribute to the refinement of clinical guidance and public health strategies to reduce infection-related complications from dog- and cat-bites.

Most patients in this cohort received empirical antibiotic treatment before mNGS sampling. Although antibiotic exposure may reduce the microbial load and alter the microbial community composition, the major pathogenic microorganisms associated with persistent wound infection can still be detected using mNGS. These findings suggest that antibiotic pretreatment may have a limited impact on overall pathogen identification, despite its potential effects on relative microbial abundance. This further highlights the clinical value of mNGS in detecting potentially resistant, anaerobic, and uncommon pathogens in persistent bite-wound infections.

This study had several limitations. First, this was a retrospective, single-center study with a relatively moderate sample size. Second, the lack of a non-animal traumatic wound control group limited our ability to distinguish animal-specific oral flora from environmental and skin contaminants. Because some opportunistic microorganisms may also originate from skin colonization or environmental exposure, the absence of an appropriate traumatic wound control group limits further assessment of the specificity of the identified microbial profiles. Future controlled comparative studies including non-animal traumatic wound infections are needed to better define the animal-associated microbial spectrum. Third, pathogen detection was performed at the molecular level without antimicrobial susceptibility testing or direct correlation with treatment outcomes. Future studies integrating microbial sequencing, drug susceptibility testing, and clinical follow-ups may clarify the clinical significance of different pathogens in bite-wound infections.

In conclusion, infected dog and cat bite wounds harbor distinct polymicrobial communities in which anaerobic bacteria are consistently predominant. These findings may help optimize empirical antimicrobial strategies and improve the clinical management of

animal bite-wound infections.

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REFERENCES

1. Lauer EA, White WC, Lauer BA. Dog bites: a neglected problem in accident prevention. *Am J Dis Child* 1982;136(3):202 – 4. <https://doi.org/10.1001/archpedi.1982.03970390016003>.
2. Douglas LG. Bite wounds. *Am Fam Physician* 1975;11:93-9. <https://pubmed.ncbi.nlm.nih.gov/1168014/>.
3. Aghababian RV, Conte JE Jr. Mammalian bite wounds. *Ann Emerg Med* 1980;9(2):79 – 83. [https://doi.org/10.1016/S0196-0644\(80\)80335-0](https://doi.org/10.1016/S0196-0644(80)80335-0).
4. Thomas PR, Buntine JA. Man's best friend?: a review of the Austin Hospital's experience with dog bites. *Med J Aust* 1987;147(11-12):536 – 40. <https://doi.org/10.5694/j.1326-5377.1987.tb133676.x>.
5. Elenbaas RM, McNabney WK, Robinson WA. Evaluation of prophylactic oxacillin in cat bite wounds. *Ann Emerg Med* 1984;13(3):155 – 7. [https://doi.org/10.1016/S0196-0644\(84\)80604-6](https://doi.org/10.1016/S0196-0644(84)80604-6).
6. Skurka J, Willert C, Yogeve R. Wound infection following dog bite despite prophylactic penicillin. *Infection* 1986;14(3):134 – 5. <https://doi.org/10.1007/BF01643478>.
7. Cummings P. Antibiotics to prevent infection in patients with dog bite wounds: a meta-analysis of randomized trials. *Ann Emerg Med* 1994;23(3):535 – 40. [https://doi.org/10.1016/S0196-0644\(94\)70073-7](https://doi.org/10.1016/S0196-0644(94)70073-7).
8. Ki V, Rotstein C. Bacterial skin and soft tissue infections in adults: a review of their epidemiology, pathogenesis, diagnosis, treatment and site of care. *Can J Infect Dis Med Microbiol* 2008;19(2):173 – 84. <https://doi.org/10.1155/2008/846453>.
9. Ortiz DD, Lezcano FO. Dog and cat bites: rapid evidence review. *Am Fam Physician* 2023;108(5):501-5. <https://www.aafp.org/afp/2023/1100/dog-cat-bites.pdf>.
10. Dougas G, Katerelos P, Chatzianastasiou S, Mellou K. The epidemiology of dog bite injuries in Greece: preliminary results of a surveillance scheme. *Hippokratia* 2023;27(3):82-8. <https://pmc.ncbi.nlm.nih.gov/articles/PMC11305156/>.
11. Babovic N, Cayci C, Carlsen BT. Cat bite infections of the hand: assessment of morbidity and predictors of severe infection. *J Hand Surg* 2014;39(2):286 – 90. <https://doi.org/10.1016/j.jhsa.2013.11.003>.
12. Liu YS, Qin SB, Lan CH, Huang QM, Zhang P, Cao WL.

- Effectiveness of metagenomic next-generation sequencing in the diagnosis of infectious diseases: a systematic review and meta-analysis. *Int J Infect Dis* 2024;142:106996. <https://doi.org/10.1016/j.ijid.2024.106996>.
13. Talan DA, Citron DM, Abrahamian FM, Moran GJ, Goldstein EJC. Bacteriologic analysis of infected dog and cat bites. *N Engl J Med* 1999;340(2):85 – 92. <https://doi.org/10.1056/NEJM199901143400202>.
 14. Rothe K, Tsokos M, Handrick W. Animal and human bite wounds. *Dtsch Arztebl Int* 2015;112(25):433 – 42. <https://doi.org/10.3238/arztebl.2015.0433>.
 15. Razali K, Kaidi R, Abdelli A, Menoueri MN, Ait-Oudhia K. Oral flora of stray dogs and cats in Algeria: Pasteurella and other zoonotic bacteria. *Vet World* 2020;13(12):2806 – 14. <https://doi.org/10.14202/vetworld.2020.2806-2814>.
 16. López-Pintor JM, García-Fernández S, Ponce-Alonso M, Sánchez-Díaz AM, Ruiz-Garbajosa P, Morosini MI, et al. Etiology and antimicrobial susceptibility profiles of anaerobic bacteria isolated from clinical samples in a University Hospital in Madrid, Spain. *Anaerobe* 2021;72:102446. <https://doi.org/10.1016/j.anaerobe.2021.102446>.
 17. Pardo-Peláez B, Sarmiento-García A. Microbiology of infections caused by dog and cat bites: a review. *Rev Chilena Infectol* 2021;38(3):393 – 400. <https://doi.org/10.4067/s0716-10182021000300393>.

SUPPLEMENTARY MATERIALS

SUPPLEMENTARY TABLE S1. Distribution of fungal pathogens detected in dog and cat bite wound specimens using mNGS.

Fungal species	Dog bites (n)	Cat bites (n)	Domestic animals (n)	Stray animals (n)
<i>Candida parapsilosis</i>	1	2	1	2
<i>Aspergillus sydowii</i>	1	1	1	1
<i>Malassezia restricta</i>	2	2	0	4
<i>Malassezia japonica</i>	1	0	0	1
<i>Malassezia globosa</i>	1	0	1	0
<i>Pichia guilliermondii</i>	0	1	1	0

Note: Only fungal pathogens detected in at least one specimen are shown. Multiple fungal pathogens could be detected in the same specimen.

Abbreviation: mNGS=metagenomic next-generation sequencing.