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Microbiology of Animal Bite Wound Infections

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INTRODUCTION

The sustained and worldwide epidemic of animal bite injuries and infections has been the subject of many scholarly reviews, and there has been a plethora of series and case reports but very few systematic studies. Since human-animal contact is a daily occurrence for most people worldwide in various settings, from farms to domestic pets to feral animals, it is not surprising that as a result of this contact, bite injuries are caused by a wide variety of domestic and wild animals. Most of these wounds are minor injuries and go unreported, and patients self-administer first aid and often do not seek or require medical attention. In industrialized countries, most patients with moderate to severe bite injuries will seek some form of medical attention whether in an emergency department or in a physician's office. When these injuries are reported, the authors of the reports generally concentrate on unusual or resistant organisms or unusual complications and their management. These retrospective incidents form the basis for anecdotal medical decision-making that is employed worldwide.

Very few studies have been systematic and have attempted to define the presentation, epidemiology, bacteriology, and/or therapy of bite wounds. However, even these systematic studies

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are generally limited to dog or cat bites and involve relatively small numbers of patients, and one must often extrapolate the best form of antimicrobial therapy to employ. One principle that has emerged and is scientifically established is that the bacteria recovered from bite wounds are reflective of the oral flora of the biting animal. In a minority of cases the pathogenic bacteria come from the victim's own skin, often as secondary invaders, or from the physical environment at the time of injury. Thus, bites by aquatic animals have a bacteriology that is reflective of their water environment. A second established principle is that the oral flora of the biting animal not only contains the usual "normal flora" but also is influenced by the microbiome of their ingested prey and other foods. Some of these isolates may be transient, while others are persistent and remain. Most individual elements of bite wound care come from localized "standards of care" or general applications of wound care principles but have never been further validated.

In an attempt to make some sense of the status of the bacteriology of animal bite wounds in humans, excluding human bites, we have attempted to review the literature using computer-assisted database searches, references from cited articles, and personal experience. By no means have we found or cited every reference, and there must be a variety of other animal bite wounds reported that we have not included. Our hope is that readers will reply with correspondence to fill in any voids in our review.

MICROBIOLOGY

Mammals

Dogs. The microbiology of infected bite wounds from dogs is similar to that of the organisms that colonize the dog's oral cavity (7, 23, 85, 90, 91, 93, 96, 192, 195). Less frequently, isolates may also come from the environment and patients' skin. Both clinically infected and early-presenting (less than 8 h postinjury and/or not yet clinically infected) dog bite wounds are polymicrobial, with a broad combination of aerobic and anaerobic microorganisms (23, 91, 92, 96, 171, 206).

The clinical presentation and microbiology of clinically infected dog bite wounds in patients without prior antibiotic exposure were studied by Talan et al. (206). This was a multicenter, prospective trial of 50 dog bite wounds, of which 60% were punctures, 10% were lacerations, and 30% were a combination of both. A majority of the infections were purulent wounds without abscess formation (58%), followed by nonpurulent wounds with cellulitis, lymphangitis, or both (30%) and abscesses (12%). An abscess was defined as a fluctuant lesion that required incision and drainage for treatment.

The numbers of bacterial isolates varied depending on the type of wound. The highest numbers of bacterial isolates obtained from cultures were from abscesses (median, 7.5; range, 2 to 11; interquartile range, 3 to 10), followed by purulent wounds (median, 5.0; range, 0 to 16; interquartile range, 2 to 11) and nonpurulent wounds (median, 2.0; range, 0 to 9; interquartile range, 1 to 4). A majority (48%) of the dog bite wounds were polymicrobial, with a mix of aerobic and anaerobic organisms. Pure aerobic growth occurred in 42% of the cases, and only one case among the abscess group demonstrated pure anaerobic growth with *Bacteroides tectus* and *Porphyromonas gulae* (previously *Porphyromonas gingivalis*).

TABLE 1. Common aerobic and anaerobic bacterial genera isolated from 50 infected dog bite wounds[a]

Bacterial genus	Frequency (%)
Aerobic organisms	
Pasteurella	50
Streptococcus	46
Staphylococcus	46
Neisseria[b]	32
Corynebacterium	12
Moraxella	10
Enterococcus	10
Bacillus	8
Anaerobic organisms	
Fusobacterium	32
Porphyromonas	28
Prevotella	28
Propionibacterium	20
Bacteroides[b]	18
Peptostreptococcus	16

[a] Based on data from reference 206.
[b] The frequencies differ from the actual numbers cited in the reference due to the reclassification of some of the isolates since its publication.

With respect to the type of wound, mixed aerobic and anaerobic infections were most common among abscesses (67%), followed by purulent wounds (62%) and nonpurulent wounds (13%). Pure aerobic growth was seen most commonly in nonpurulent wounds but with associated cellulitis/lymphangitis (67%), followed by purulent wounds (34%) and abscesses (17%). No growth on culture media occurred for only four patients (8%). For three of these patients, their wounds were described as being a nonpurulent wound with cellulitis, lymphangitis, or both, and the remaining one patient had a purulent wound. No cultures were done for mycobacteria, *Chlamydia*, *Mycoplasma*, or viruses.

(i) Aerobes. Table 1 shows common aerobic bacterial genera isolated from 50 infected dog bite wounds (206). In this multicenter study, the most common aerobic organisms isolated at a research laboratory were *Pasteurella* (50%), *Streptococcus* (46%), *Staphylococcus* (46%), *Neisseria* (32%), and *Corynebacterium* (12%) species. Other aerobic organisms, in order of decreasing frequency, included *Moraxella* species (10%), *Enterococcus* species (10%), *Bacillus* species (8%), *Pseudomonas* species (6%), *Actinomyces* species (6%), *Brevibacterium* species (6%), *Gemella morbillorum* (6%), *Escherichia coli* (6%), *Weeksella zoohelcum* (4%), *Klebsiella* species (4%), *Lactobacillus* species (4%), *Citrobacter* species (4%), *Flavobacterium* species (4%), *Micrococcus* species (4%), *Proteus mirabilis* (4%), *Stenotrophomonas maltophilia* (4%), *Capnocytophaga ochracea* (2%), *Eikenella corrodens* (2%), *Flavimonas oryzihabitans* (2%), *Dermabacter hominis* (2%), *Oerskovia* species (2%), *Pediococcus damnosus* (2%), and *Stomatococcus mucilaginosus* (2%).

Among members of the genus *Pasteurella*, *Pasteurella canis* was the most common species isolated from infected dog bite wounds (26%) (206). Others, in order of deceasing frequency, included *Pasteurella multocida* subsp. *multocida* (12%), *Pasteurella stomatis* (12%), *Pasteurella multocida* subsp. *septica* (10%), *Pasteurella dagmatis* (4%), and *Pasteurella multocida*

subsp. *gallicida* (2%). *Pasteurella multocida* subsp. *multocida* and subsp. *septica* have been implicated in more serious systemic infections, with *Pasteurella multocida* subsp. *septica* having a tendency to result in central nervous system infections (15, 91, 92, 115, 183). In comparison to staphylococci or streptococci, the isolation of *Pasteurella* species is commonly associated with a shorter latency period, which is defined as the time from the bite to the appearance of the first symptoms of infection (1, 206, 212, 230). Other observations have included finding *Pasteurella* more frequently in abscesses, nonpurulent wounds with lymphangitis, puncture wounds, and bites involving the upper extremities than from bites involving the lower extremities (206).

Although *Pasteurella* has been recovered from many other animals (10, 19, 25, 76, 87, 122, 136, 148, 237), including birds (32, 110), in a study of 146 human infections with *Pasteurella* species, *Pasteurella canis* (biotype 1) was associated exclusively with dog bites (115). The higher prevalence of *Pasteurella canis* in dogs was also observed in a study of *Pasteurella* strains involving various animal hosts (15). Some species of *Pasteurella* are capable of producing toxins, such as *Pasteurella multocida* subsp. *multocida* and *Pasteurella canis* (115, 167); however, the role of toxin production, the mechanism of action in the pathogenicity of human diseases, and its clinical relevance are not clearly understood. Toxin-producing *Pasteurella* strains have been reported for minor wound infections (115).

The second most common species isolated from dog bite wounds in equal frequencies were *Streptococcus* and *Staphylococcus* species (206). The prevalence of these two species was notably more common in nonpurulent wounds with cellulitis/lymphangitis than in abscesses or purulent wounds (206). Among members of the genus *Streptococcus*, the most common species isolated was *Streptococcus mitis* (22%). Other species, in order of decreasing frequency, included *Streptococcus mutans* (12%), *Streptococcus pyogenes* (12%), *Streptococcus sanguis* biotype II (8%), *Streptococcus intermedius* (6%), *Streptococcus constellatus* (4%), *Streptococcus equinus* (2%), *Streptococcus sanguis* biotype I (2%), *Streptococcus agalactiae* (2%), *Streptococcus sanguis* (2%), beta-hemolytic *Streptococcus* group G (2%), and *Streptococcus dysgalactiae* (2%).

Among staphylococci, *Staphylococcus aureus* was the most common species isolated (20%), followed by *Staphylococcus epidermidis* (18%) and *Staphylococcus warneri* (6%). Other less commonly isolated staphylococci included *Staphylococcus intermedius* (2%), *Staphylococcus hominis* (2%), *Staphylococcus auricularis* (2%), *Staphylococcus cohnii* (2%), and *Staphylococcus xylosus* (2%). β-Lactamase production is common among strains of staphylococci isolated from infected bites (206).

Canine gingival cultures were obtained from 135 healthy dogs at an urban veterinary clinic in Santa Monica, CA, 10% of which grew *Staphylococcus aureus* and were associated with dogs of working breeds with weights greater than 40 lb and outdoor habitats (209). In that same study, *Staphylococcus intermedius* was isolated in 39% of cultures and was associated with dogs from nonworking breeds with weights less than 40 lb and indoor habitats. *Staphylococcus aureus* and *Staphylococcus intermedius* were concomitantly isolated in only three dogs (2%) (209).

Staphylococcus intermedius may mistakenly be identified as *Staphylococcus aureus*, since both are coagulase positive (206, 208). Its features that distinguish it from *Staphylococcus aureus* include its β-galactosidase activity and the lack of acetoin production (209). *Staphylococcus intermedius* also demonstrates a high level of phenotypic similarity to *Staphylococcus pseudintermedius* (8, 58). Genetically, it was shown that the *Staphylococcus intermedius* group consists of three distinct species, *Staphylococcus intermedius*, *Staphylococcus pseudintermedius*, and *Staphylococcus delphini* (8). The distinction among these species is difficult with routine diagnostic bacteriology, and confirmation requires molecular techniques (8). The discovery of the *Staphylococcus intermedius* group and its three distinct species has led to *Staphylococcus pseudintermedius*, not *Staphylococcus intermedius*, becoming a common cause of canine skin infections (8, 57, 75, 80).

In addition, *Staphylococcus intermedius* may also be incorrectly identified as methicillin-resistant *Staphylococcus aureus* (MRSA). Reports of such misidentification have occurred when the penicillin binding protein 2a latex agglutination test was used to detect methicillin resistance (179). *Staphylococcus intermedius* is often susceptible to oxacillin (209); however, reports of oxacillin-resistant strains have been made (111). Conclusive identification may require molecular techniques such as PCR and the demonstration of the absence of the *mecA* gene (179). MRSA-associated infections, commonly linked with orthopedic surgeries, have been reported for dogs and other animals (51, 169, 174, 182, 213). The transmission and carriage of identical strains of MRSA (including Panton-Valentine leucocidin-positive strains) between humans and dogs have also been demonstrated through genetic and molecular techniques (9, 33, 154, 222, 223). We are not aware of any reports of MRSA isolated from an infected dog bite wound in a human.

Neisseria and *Corynebacterium* species were also commonly found in samples from dog bite wounds (4, 206). The most commonly found *Neisseria* species was *Neisseria weaveri* (14%) (formerly known as CDC group M-5), followed by *Neisseria zoodegmatis* (10%) (formerly known as EF-4b), *Neisseria animaloris* (6%) (formerly known as EF-4a), and *Neisseria subflava* (2%). Among *Corynebacterium* species, the most commonly isolated species were *Corynebacterium* group G (6%) and *Corynebacterium minutissimum* (4%). Less frequently observed corynebacterial isolates were *Corynebacterium aquaticum* (also known as *Leifsonia aquaticum*), *Corynebacterium jeikeium*, *Corynebacterium afermentans*, *Corynebacterium* group E, and *Corynebacterium pseudodiphtheriticum*. In a recent case report, *Corynebacterium freiburgense* was isolated from a human wound inflicted by a dog (83).

Species that were present ≤10% of the time included *Moraxella* isolates not identified to the species level (10%) (isolates could not be identified beyond the genus level), *Enterococcus faecalis* (6%), *Brevibacterium* (6%) (isolates could not be identified beyond the genus level), *Gemella morbillorum* (6%), *Escherichia coli* (6%), *Bacillus firmus* (4%), *Actinomyces viscosus* (4%), *Proteus mirabilis* (4%), *Stenotrophomonas maltophilia* (4%), and *Bergeyella zoohelcum* (4%) (previously known as *Weeksella zoohelcum* and prior to that known as CDC group IIj) (206). *Bergeyella zoohelcum* is likely to be an opportunistic pathogen (202) and has been reported in association with various clinical syndromes, including meningitis, bacteremia, and abscess formation after a dog bite (20, 161, 187).

Less commonly observed (≤2%) organisms included

Moraxella catarrhalis, *Enterococcus avium*, *Enterococcus malodoratus*, *Bacillus circulans*, *Bacillus subtilis*, *Pseudomonas aeruginosa*, *Pseudomonas vesicularis*, *Pseudomonas diminuta*, *Actinomyces neuii* subsp. *anitratus*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Lactobacillus lactis*, *Citrobacter amalonaticus*, *Citrobacter koseri*, *Flavobacterium* group IIa, *Flavobacterium brevis*, *Micrococcus lylae*, *Capnocytophaga ochracea*, *Eikenella corrodens*, *Flavimonas oryzihabitans*, *Dermabacter hominis*, *Oerskovia* species, *Pediococcus damnosus*, and *Stomatococcus mucilaginosus* (206).

Capnocytophaga canimorsus has been implicated as a pathogenic agent in a variety of clinical conditions such as septicemia, purpura fulminans, peripheral gangrene, endocarditis, and meningitis following dog bites (116, 139, 158, 166, 178, 189). Although fulminant infections with *Capnocytophaga canimorsus* after a dog bite have been reported for immunocompetent patients (116), it appears that immunocompromised patients (e.g., those who have undergone splenectomy and those with liver disease, etc.) are most susceptible to this type of infection and its complications (139, 166, 178, 189). *Capnocytophaga canimorsus* (formerly known as CDC group DF-2) is a fastidious organism, and growth in blood cultures often takes days (mean, 6 days; range, 1 to 14 days) (139). Growth on blood or chocolate agar is significantly improved when culturing is performed in a CO_2-enriched atmosphere (22, 116). MacConkey or triple-sugar-iron agars do not support *Capnocytophaga canimorsus* growth (22). It has been recommended that horse blood agar plates with Difco blood agar base 2 support the growth of *Capnocytophaga canimorsus* better than chocolate agar (178). Examination of the Gram stain of buffy coat preparations or samples obtained from petechial lesions was suggested to be a useful rapid diagnostic test for the identification of *Capnocytophaga canimorsus* (109, 139, 158).

Less commonly reported than *Capnocytophaga canimorsus*, *Capnocytophaga cynodegmi* (formerly known as CDC group DF-2-like) was also reported to result in infections following dog bites (22, 197). Distinguishing these two organisms from one another is often difficult and requires species-specific molecular-based detection systems (205). Although both *Capnocytophaga canimorsus* and *Capnocytophaga cynodegmi* share several characteristics with *Capnocytophaga* species, they differ genetically from other members of *Capnocytophaga* species (e.g., *Capnocytophaga ochracea*, *Capnocytophaga gingivalis*, and *Capnocytophaga sputigena*) (22). Biochemical reactions useful in differentiating *Capnocytophaga canimorsus* and *Capnocytophaga cynodegmi* from other *Capnocytophaga* species include positive oxidase and catalase reactions with *Capnocytophaga canimorsus* and *Capnocytophaga cynodegmi* (22).

(ii) Anaerobes. Table 1 shows common anaerobic bacterial genera isolated from 50 infected dog bite wounds (206). The most common anaerobic organisms, in order of decreasing frequency, included *Fusobacterium nucleatum* (16%), *Bacteroides tectus* (14%), *Prevotella heparinolytica* (14%), *Propionibacterium acnes* (14%), *Prevotella intermedia* (8%), *Peptostreptococcus anaerobius* (8%), *Porphyromonas macacae* (6%), and *Porphyromonas cansulci* (6%) (206). Pure anaerobic growth is rare and is almost always accompanied by aerobic organisms (96, 206). β-Lactamase production is a common feature among anaerobes isolated from infected bites (23, 206). Anaerobes are commonly present in abscesses, puncture wounds, and upper extremity wounds (206). The growth and identification of anaerobic organisms are frequently a difficult task. In comparison to research laboratories, local hospital laboratories are not often able to grow the majority of anaerobic organisms (206). This limitation may erroneously lead clinicians to believe that there is an absence of these organisms in infected wounds. In addition, some anaerobic isolates such as those belonging to the genera *Bacteroides* and *Prevotella* (e.g., *Bacteroides tectus* and *Prevotella bivia* or *Prevotella heparinolytica* and *Bacteroides uniformis*) have a close resemblance in colony morphology and biochemical activity, hence making their distinction from one another more difficult (3). Primary culture often requires longer incubation periods, good anaerobic media, and biochemical tests. In order to increase the yield of anaerobes, it has been recommended that laboratories retain inoculated anaerobic plates from bite wounds for at least 7 days (42).

Less commonly observed (≤4%) anaerobic isolates include *Tannerella forsythia* (previously *Bacteroides forsythus*), *Campylobacter gracilis* (previously *Bacteroides gracilis*), *Campylobacter ureolyticus* (previously *Bacteroides ureolyticus*), *Porphyromonas canoris*, *Porphyromonas cangingivalis*, *Prevotella zoogleoformans*, *Eubacterium* species (isolates were not identified beyond the genus level), *Fusobacterium russii*, *Fusobacterium gonidiaformans*, *Fusobacterium alocis*, *Bacteroides tectus* group E, *Bacteroides fragilis*, *Bacteroides ovatus*, *Porphyromonas circumdentaria*, *Porphyromonas levii*-like, *Prevotella melaninogenica*, *Prevotella denticola*, *Propionibacterium acidipropionici*, *Propionibacterium freudenreichii*, *Peptostreptococcus asaccharolyticus*, and *Lactobacillus jensenii* (206, 220).

Other organisms isolated from infected dog bites have included *Veillonella parvula* (96), *Porphyromonas salivosa* (42, 118), *Prevotella bivia* (3), and the newly described *Fusobacterium canifelinum*, which are intrinsically resistant to fluoroquinolones due to the replacement of Ser79 with leucine and the replacement of Gly83 with arginine in the quinolone resistance-determining region (*gyrA*) (46, 47).

Cats. The microbiology of infected human cat bite wounds is similar to that of wounds inflicted by dogs in that both are polymicrobial in nature (23, 96, 206). In a multicenter prospective study of 57 clinically infected human cat bite wounds (206), 63% of the wounds were a mix of aerobic and anaerobic organisms. Pure aerobic growth occurred in 32% of the cases, and none demonstrated pure anaerobic growth. Only three (5%) of the cultures resulted in no growth (one from a patient with a purulent wound and two from patients with nonpurulent wounds but associated cellulitis/lymphangitis).

The most common type of infection was a nonpurulent wound with cellulitis, lymphangitis, or both (42%), followed by a purulent wound without abscess formation (39%) and abscesses (19%). Mixed aerobic and anaerobic infections were most common among abscesses (73%), followed by purulent wounds (64%) and nonpurulent wounds (58%) (206).

The number of bacterial isolates varied depending on the type of wound. The highest numbers of bacterial isolates were from abscesses (median, 7.0; range, 3 to 13; interquartile range, 5 to 11), followed by purulent wounds (median, 6.5; range, 0 to 13; interquartile range, 3 to 10) and nonpurulent wounds (median, 5.0; range, 0 to 12; interquartile range, 2 to 6). The majority (85%) of injuries were described as being

TABLE 2. Common aerobic and anaerobic bacterial genera isolated from 57 infected cat bite wounds[a]

Bacterial genus	Frequency (%)
Aerobic organisms	
Pasteurella	75
Streptococcus	46
Staphylococcus	35
Neisseria[b]	35
Moraxella	35
Corynebacterium	28
Enterococcus	12
Bacillus	11
Anaerobic organisms	
Fusobacterium	33
Porphyromonas	30
Bacteroides	28
Prevotella	19
Propionibacterium	18

[a] Based on data from reference 206.
[b] The frequency differs from the actual number cited in the reference due to the reclassification of some of the isolates since its publication.

puncture wounds, while the rest were lacerations (3%) or mixes of both lacerations and puncture wounds (12%). In comparison to dog bites, the median time from the bite to the appearance of the first symptoms of infection was significantly shorter for cat bites (12 h; interquartile range, 7 to 18 versus 24 h; interquartile range, 12 to 48 h; $P < 0.001$) (206).

(i) Aerobes. Table 2 shows common aerobic bacterial genera isolated from 57 infected cat bite wounds (206). *Pasteurella* was the genus most commonly found for cat bite wounds, with *Pasteurella multocida* subsp. *multocida* (54%) and *Pasteurella multocida* subsp. *septica* (28%) being the predominant *Pasteurella* isolates. The predominance of these two *Pasteurella* strains in cat bites has also been observed by other studies (15, 115). Other less frequently found isolates included *Pasteurella dagmatis* (7%), *Pasteurella stomatis* (4%), and *Pasteurella canis* (2%) (206). *Pasteurella multocida* has also been reported for numerous human infections following bites of larger cats such as tigers (25, 122, 237), lions (25), and cougars (136).

Streptococci were the second most common species isolated from cat bite wounds (206). *Streptococcus mitis* was also the most common *Streptococcus* species isolated from both types of animal bite wounds (23% in cats and 22% in dogs) (206). Other species found in cat bite wounds included *Streptococcus sanguis* biotype II (12%), *Streptococcus mutans* (11%), *Streptococcus equinus* (5%), *Streptococcus sanguis* biotype I (5%), *Streptococcus intermedius* (4%), *Streptococcus constellatus* (4%), *Streptococcus agalactiae* (2%), *Streptococcus sanguis* (2%), and beta-hemolytic *Streptococcus* group F (2%). Among dog and cat bite wounds, the majority of *Streptococcus* isolates shared a similar frequency of occurrence, with the exception of *Streptococcus pyogenes*, which was not seen in cat bite wounds (12% prevalence for dog bites) (206).

In equal frequency, staphylococci, *Neisseria*, and *Moraxella* were the next most common genera found in cat bite wounds. The most common staphylococcal isolates were *Staphylococcus epidermidis* (18%) and *Staphylococcus warneri* (11%). Other less frequently found isolates were *Staphylococcus aureus* (4%), *Staphylococcus sciuri* subsp. *lentus* (4%), *Staphylococcus intermedius* (2%), *Staphylococcus hominis* (2%), *Staphylococcus capitis* (2%), *Staphylococcus haemolyticus* (2%), *Staphylococcus hyicus* (2%), *Staphylococcus saprophyticus* (2%), and *Staphylococcus simulans* (2%). In comparison, *Staphylococcus aureus* was less frequently observed for cat bites than for dog bites (4% versus 20%) (206). Among *Neisseria* species, *Neisseria weaveri* (14%) (formerly known as CDC group M-5) was the most common *Neisseria* species, followed by *Neisseria zoodegmatis* (9%) (formerly known as EF-4b), *Neisseria subflava* (2%), *Neisseria cinerea-Neisseria flavescens* (2%), and *Neisseria mucosa* (2%). There were no significant differences in the prevalences of the various *Neisseria* isolates between cat and dog bite wounds (206). Human infections after a cat bite associated with *Neisseria canis* have also been reported (104, 113). Among *Moraxella* species, *Moraxella catarrhalis* was the most commonly found identifiable isolate. Most others were not identified beyond the genus level. *Moraxella catarrhalis* was found more often in cat bite wounds than in dog bite wounds (11% versus 2%) (206).

For *Corynebacterium* species, the most commonly isolated species were *Corynebacterium* (*Leifsonia*) *aquaticum* (14%), *Corynebacterium minutissimum* (7%), and *Corynebacterium* group G (5%). Less frequently observed corynebacterium isolates included *Corynebacterium jeikeium*, *Corynebacterium* group B, *Corynebacterium* group F-1, *Corynebacterium kutscheri* (2%), *Corynebacterium propinquum* (2%), and *Corynebacterium striatum* (2%). *Corynebacterium* (*Leifsonia*) *aquaticum* was more prevalent in cat bites than in dog bites (14% versus 2%). *Enterococcus durans* (9%) (none isolated from dog bites) and *Enterococcus faecalis* (4%) were the most commonly found enterococcal isolates. *Bacillus firmus* (4%) and *Bacillus circulans* were the most commonly found identifiable bacillus isolates (206).

Less frequently encountered aerobic organisms, in order of decreasing frequency, included *Bergeyella zoohelcum* (7%) (previously known as *Weeksella zoohelcum* and prior to that known as CDC group IIj), *Capnocytophaga* species (7%), *Acinetobacter* species (7%), *Pseudomonas* species (5%), *Actinomyces* species (4%), *Brevibacterium* species (4%), *Gemella morbillorum* (4%), *Actinobacillus* species (4%), *Alcaligenes* species (4%), *Enterobacter cloacae* (4%), *Erysipelothrix rhusiopathiae* (4%), *Riemerella anatipestifer* (4%), *Rothia dentocariosa* (4%), *Klebsiella oxytoca* (2%), *Lactobacillus* species (2%), *Eikenella corrodens* (2%), *Flavimonas oryzihabitans* (2%), *Aeromonas hydrophila* (2%), *Pantoea agglomerans* (2%), *Rhodococcus* species (2%), and *Streptomyces* species (2%) (206).

Infection with *Bergeyella zoohelcum* was reported for a case of cellulitis after a cat bite (202). In that report, the strain was unusually fastidious and did not yield sufficient growth for identification using standard culture methods and required molecular techniques (PCR with rRNA gene sequencing) for identification. The use of the MicroSeq 500 16S rRNA gene-based bacterial identification system has resulted in the misidentification of *Bergeyella zoohelcum* as *Riemerella anatipestifer* (236). *Bergeyella zoohelcum* was also reported to result in tenosynovitis associated with *Pasteurella multocida* and other Gram-negative bacteria after a bite from a Siberian tiger (122). *Capnocytophaga canimorsus* (formerly known as CDC group DF-2) has been implicated in severe infections following cat bites or exposure (31, 217, 234). Newly discovered organisms in

cats include *Haemophilus felis*, initially identified as *Aggregatibacter* (*Haemophilus*) *paraphrophilus* (121), and a novel biotype of *Corynebacterium diphtheriae* (105). Their pathogenicity and potential for transmission to humans are unknown.

Cats are also the main reservoir of *Bartonella henselae*, the causative agent of cat scratch disease (190). Most patients with cat scratch disease report a history of a scratch or a bite by a cat (155, 240). The transmission of *Bartonella henselae* to cats is vector mediated through the cat flea, *Ctenocephalides felis* (41). Due to its fastidious nature, *Bartonella henselae* growth and isolation can be very difficult. Various culture media (e.g., rabbit blood and chocolate agars), the serological detection of *Bartonella henselae* antibodies by an indirect immunofluorescent assay, and other molecular techniques such as PCR are often utilized for its identification (54, 55, 56, 190). Another *Bartonella* species recently implicated in the development of cat scratch disease due to a cat bite is *Bartonella clarridgeiae* (138). This species should also be considered a potential agent of cat scratch disease, especially for patients who demonstrate negative seroreactivity against *Bartonella henselae*. The spectrum of cat scratch disease can range from regional tender lymphadenopathy to, less commonly, fulminant systemic infections, osteomyelitis, and encephalopathy (5, 153, 190, 235).

(ii) Anaerobes. Table 2 shows common anaerobic bacterial genera isolated from 57 infected cat bite wounds (206). In this case series, anaerobes were almost always isolated in mixed cultures along with aerobic organisms, and none of the wound specimens demonstrated pure anaerobic growth (206).

Fusobacterium nucleatum prevailed as the most commonly found *Fusobacterium* isolate from cat bites (25%). Other isolates found in cat bites included *Fusobacterium russii* (14%) and *Fusobacterium gonidiaformans* (2%). The prevalence of *Fusobacterium russii* was significantly higher in cat bites than in dog bites (14% versus 2%). The most common *Porphyromonas* isolate in cat bites was *Porphyromonas gulae* (11%). Other isolates included *Porphyromonas canoris* (9%), *Porphyromonas macacae* (7%), *Porphyromonas circumdentaria* (5%), *Porphyromonas cangingivalis* (4%), and *Porphyromonas cansulci* (2%). There were no significant prevalence differences among the various *Porphyromonas* species in dog and cat bite wounds. *Bacteroides tectus* was the main *Bacteroides* species isolated from both dog and cat bites (14% in dog bites and 28% in cat bites). Other *Bacteroides* isolates were *Bacteroides tectus* group E (4%) and *Bacteroides fragilis* (2%) (206).

Among *Prevotella* species, *Prevotella heparinolytica* was the most commonly found isolate in both dog and cat bite wounds (14% in dog bites and 9% in cat bites). Other *Prevotella* isolates less frequently encountered were *Prevotella zoogleoformans* (2%) and *Prevotella melaninogenica* (2%). Within the genus *Propionibacterium*, *Propionibacterium acnes* dominated in both dog and cat bite wounds (14% in dog bites and 16% in cat bites). Other *Propionibacterium* isolates were *Propionibacterium avidum* (2%) and *Propionibacterium lymphophilum* (2%). Less frequently encountered anaerobes included *Peptostreptococcus anaerobius* (5%), *Filifactor villosus* (5%), *Eubacterium* species (2%) (could not be identified beyond the genus level), *Clostridium sordellii* (2%), and *Veillonella* species (2%) (were not identified beyond the genus level) (206).

Rare infectious diseases in humans acquired from cats and dogs. (i) Cats. Cat and other feline bites and exposures have been associated with the human transmission of *Francisella tularensis* resulting in tularemia (6, 28, 73, 225, 231). The role of cats, especially those that are free-roaming, is increasingly being recognized as one probable mode of transmission of *Yersinia pestis* and a source of human plague (34, 38, 48, 60, 84, 99, 232, 233). Infections following bites, scratches, and contact with infectious materials as well as the inhalation of infectious aerosol while examining an infected cat have been reported (34, 84, 232, 233). The presentation of pet-associated human plague has included bubonic (34, 48, 84, 232), septicemic (48, 84), and pneumonic (34, 60, 84, 233) forms. In a review of human cases of plague in the United States from 1977 to 1994, the prevalence of primary pneumonic plaque was higher among cat-associated cases (4 cases out of 15) than among other cases associated with mammals that transmit plaque (1 out of 236) (34).

The transmission of *Sporothrix schenckii* to humans from cats has been widely reported (11, 53, 62, 77, 81, 144, 185, 186, 199, 239) and confirmed at the genetic level (186). Infections following a bite or scratch and even in instances without an obvious penetrating injury have been reported (53, 62, 77, 186, 199). Household outbreaks and epidemics of sporotrichosis involving cats and humans have been described (11, 53, 81, 199). Most infections in humans present as localized lymphocutaneous lesions. Sporotrichosis has also been reported for dogs and other animals (49, 199); however, in contrast to cats, the zoonotic transmission of sporotrichosis to humans from other animals has not been as widely reported.

(ii) Dogs. Blastomycosis in humans acquired from dogs has also been reported (152, 198). Reports of the mode of zoonotic transmission of *Blastomyces dermatitidis* from infected dogs have included bites and accidental exposure to infected material (89, 100, 124, 181). Various *Bartonella* species DNA, including that of *Bartonella henselae*, have been isolated from dog saliva (61). *Bartonella* infection such as endocarditis has also been reported for dogs (21, 170). However, in comparison to cats, the role of dogs as a source of human *Bartonella* infection is not as well understood and is restricted to only a few non-bite-related case reports (129, 130, 216).

(iii) Cats and dogs. Rabies in domestic animals such as cats and dogs is rare in the United States. In a 2008 U.S. rabies surveillance study, the prevalences of rabies in cats and dogs were 4.3% and 1.1%, respectively. In comparison to the previous year, the number of rabies cases reported in 2008 increased among cats and decreased among dogs (17). The dog-to-dog transmission of canine rabies virus variants has been eliminated in the United States since 2004 (17). Most human rabies cases in the United States have been associated with rabid bats, while in developing countries, dogs are the most common animals implicated in the transmission of rabies to humans (39).

Monkeys/simians. Bites from monkeys may occur in people who keep them as pets, those who use them for medical research, and those who travel to cities and countries that have a high prevalence of free-roaming monkeys (e.g., Gibraltar, Bali, and certain parts of India). In addition, persons who visit or

TABLE 3. Oral bacteriology of rhesus monkeys and isolates recovered from humans with simian bite wounds

Organism	Oral bacteriology of rhesus monkey (% of isolates) determined by:		No. of patients ($n = 3$)[c]
	Rayan et al.[a] ($n = 17$)	Eke et al.[b] ($n = 9$)	
Actinomyces species		85	
Aerococcus species	2.4		
Aggregatibacter actinomycetemcomitans[d]		73	
Bacillus species	7.4		
Bacteroides fragilis group		5	1
Campylobacter species		28	
Capnocytophaga species		30	
Eikenella corrodens	1.2	4.7	1
Escherichia coli	1.2		1
Fusobacterium nucleatum		90	1
Haemophilus influenzae	1.2		
Haemophilus parainfluenzae	17.2		
Haemophilus species		100	
Klebsiella pneumoniae			1
Moraxella species	2.4		
Neisseria species	19.8		1 (*N. subflava*)
Peptostreptococcus micros		89	
Pseudomonas species	2.4		
Staphylococcus aureus	3.6		
Staphylococcus species	1.2		2 (*S. epidermidis*)
Staphylococcus, beta-hemolytic	3.8		
Alpha-hemolytic streptococci	19.8		1 (unidentified), 1 (*S. mitis*), 1 (*S. sanguis*), 1 (*S. sanguis* biotype II), 1 (*S. anginosus*), 1 (*S. intermedius*)
Beta-hemolytic streptococci			1 (*S. agalactiae*)
Nonhemolytic streptococci	1.2		2 (*E. faecalis*)
Streptococcus species	1.2		
Wolinella species		66	

[a] Based on data from reference 184.
[b] Based on data from reference 67.
[c] Based on data from reference 97.
[d] Previously known as *Actinobacillus actinomycetemcomitans*.

work in wilderness areas and national parks worldwide where monkeys reside are also at a higher risk. These animals are often considered "mischievous" and will scour for food if hungry.

Although monkey bites are commonly reported, surprisingly very few studies have investigated the bacteriology of monkey bite wounds. Kizer (135) reported that 5 out of 332 (1.7%) patients who presented to the University of California—Los Angeles (UCLA) Emergency Department during 1975 for bite wounds were inflicted by monkeys. Rates of monkey bites in facilities seeing animal bite wounds have been reported from a number of countries and range from 3.2% in India to 0.7% in Israel (72, 102, 120). In the United Kingdom, an animal housing facility reported 85 monkey bites (67 incidents in men and 18 in women) in handlers over a 6-year period (215).

The oral flora of selected monkeys and isolates from human bites is shown in Table 3. In a study of the aerobic tongue flora of 17 rhesus monkeys, commonly isolated microorganisms included *Neisseria* species (19.5%), streptococcus species (19.5%), and *Haemophilus parainfluenzae* (17.2%) (184). Another study of rhesus monkeys involving the bacteriology of gingival sulci and associated plaques revealed the following organisms colonizing the gingival sulci, in order of decreasing frequency: *Haemophilus* species (100%), *Fusobacterium nucleatum* (90%), *Peptostreptococcus micros* (89%), *Actinomyces* species (85%), oral streptococci (80%), black-pigmented anaerobic rods (80%), *Actinobacillus actinomycetemcomitans* (73%), *Wolinella* species (66%,), *Capnocytophaga* species (30%), *Campylobacter* species (28%), *Eikenella corrodens* (4.7%), and spirochetes (4.7%) (67).

The spectrum of isolates from humans bitten by monkeys is similar to that of isolates from human bite wounds. There is a predominance of alpha-hemolytic streptococci, enterococci, *Staphylococcus epidermidis*, *Neisseria* and *Haemophilus* species, *Eikenella corrodens*, and anaerobes, including *Bacteroides* and *Fusobacterium* species (97).

A major concern with monkey bites is the transmission of viral diseases. Jones-Engel et al. studied the prevalence of selected enzootic primate-borne viruses among 39 rhesus monkeys in Katmandu, Nepal (126). Evidence of infection of these monkeys through positive antibody responses to simian foamy virus (97.4%), *Cercopithecine herpesvirus 8* (94.9%), simian virus 40 (89.7%), and *Cercopithecine herpesvirus 1* (64.1%) (also known as B virus) with various molecular techniques was noted.

Documented cases of B virus infection in humans have been attributed mostly to monkey bites. However, other less commonly reported modes of transmission have been due to scratches and percutaneous inoculation with infected materials (45). A fatal case of B virus infection following mucocutaneous exposure was reported (35). Other reports of bite-related primate-borne viral infections in humans have included simian foamy virus (especially from ape bites) and monkeypox virus infections (26, 163, 200).

Bears. Bear attacks have been reported worldwide (29, 52, 106, 164, 188, 214, 227). Human injuries from grizzly bears (*Ursus arctos horribilis*) in the national parks of North America have been reported, with an injury rate of 1 person per 2 million visitors (106). From 1900 to 1985, 162 bear-inflicted injuries (~2 attacks per year) were reported for the U.S. and Canadian national parks (107). Although bear-inflicted human injuries and death are uncommon (78), as the remote bear habitat decreases and humans enter wilderness areas for living and recreation, there are more chances of encounters between bears and humans.

Data for the oral bacteriology of bears as well as bear bite wounds in humans are limited to a few studies and case reports (79, 140, 145, 175, 193). Organisms isolated from grizzly or black bear oral cavities have included *Streptococcus* (61%), *Staphylococcus* (48%), *Escherichia* (40%), *Enterobacter* (25%), *Citrobacter* (10%), *Hafnia* (10%), *Proteus* (6%), and *Acinetobacter* (6%) species (175).

The aerobic oral flora of 12 black bears (*Ursus americanus*) with periodontal disease from the northern lower peninsula of Michigan has been investigated (79). All of the cultures yielded at least one organism. In order of decreasing frequency, isolates included *Micrococcus* species (83%), alpha-hemolytic *Streptococcus* (50%), *Staphylococcus aureus* (33%), *Staphylococcus epidermidis* (16%), beta-hemolytic *Streptococcus* (16%), *Acinetobacter* species (16%), nonhemolytic *Streptococcus* (8%),

TABLE 4. Bacteria isolated from bear bite wounds in humans[a]

Bacterium isolated from bear bite wounds
Aeromonas hydrophila
Bacillus cereus
Citrobacter diversus
Enterococcus durans
Escherichia coli
Mycobacterium fortuitum
Neisseria sicca
Proteus vulgaris
Serratia fonticola
Serratia marcescens
Staphylococcus aureus
Staphylococcus epidermidis
Streptococcus sanguis

[a] Based on data from references 140, 145, and 193.

TABLE 5. Bacteria isolated from pig bite wound infections in humans[a]

Bacterium isolated from pig bite wound infections
Actinobacillus suis
Bacteroides species, including *Bacteroides fragilis*
Escherichia coli
Flavobacterium group IIb-like organism
Pasteurella aerogenes
Pasteurella multocida
Proteus species
Staphylococcus aureus (methicillin resistant)
Staphylococcus species (coagulase negative)
Streptococcus agalactiae
Streptococcus dysgalactiae

[a] Based on data from references 10, 51, 66, 70, and 95.

Bacillus species (8%), *Enterobacter* species (8%), *Klebsiella pneumoniae* (8%), *Proteus mirabilis* (8%), *Proteus* species (8%), and *Actinomyces* species (8%).

The bacteria isolated from bear bite wounds come from a number of individual care reports (Table 4). Kunimoto et al. reported a 49-year-old hunter who was attacked by a grizzly bear and sustained multiple injures, including a bite on his skull (140). Deep-wound cultures from the scalp lacerations grew *Serratia fonticola*, *Serratia marcescens*, *Aeromonas hydrophila*, *Bacillus cereus*, and *Enterococcus durans*. Anaerobic cultures did not grow any organisms. In this case report, microbiological results were limited by a delay in obtaining wound cultures (12 h after the injury) and a history of prior exposure to antibiotics (cefazolin and metronidazole). Other organisms grown from grizzly bear wounds in humans have included *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Proteus vulgaris*, *Citrobacter diversus*, and *Escherichia coli* (193). In this report, it is unclear if the injuries occurred as a result of a claw or a bite and if patients had any prior exposure to antibiotics.

Lehtinen et al. reported a case of a 56-year-old male who sustained several bite wounds from a brown bear (*Ursus arctos*) (145). Bacterial cultures from a deep thigh bite wound grew *Streptococcus sanguis*, *Neisseria sicca*, *Bacillus* species, and *Mycobacterium fortuitum*. It is unclear if anaerobic cultures were obtained from this patient or if antibiotic prophylaxis (ceftriaxone) was administered prior to obtaining would cultures.

Rabies virus infection of bears has also been reported (36). However, to our knowledge there have not been any reports of rabies transmission from bears to humans.

Pigs. Pig bite injuries are a common occupational hazard in pig farmers and can also be seen in those who keep pigs as household pets. Injuries, often on extremities, commonly occur during the capture, transport, or immobilization of the pig (10, 168, 221). Human wound infections after a pig bite have been reported in a few case reports and series (10, 66, 70, 95).

Table 5 lists the bacteria isolated from pig bite wound infections in humans. Barnham reported the microbiology of six patients who developed localized wound infections after being bitten or gored by pigs (10). Both monobacterial and polymicrobial infections were encountered. One patient did not grow any organisms from his wound or blood cultures, likely due to prior antibiotic exposure. Organisms isolated from these patients included *Streptococcus agalactiae*, *Streptococcus dysgalactiae* (likely subsp. *dysgalactiae*), *Streptococcus suis*, *Pasteurella aerogenes*, *Proteus* species, *Escherichia coli*, *Bacteroides* species including *Bacteroides fragilis*, *Pasteurella multocida*, and coagulase-negative *Staphylococcus*. In the same case series, that author also reported *Streptococcus milleri* bacteremia in a 20-year-old man who sustained a hand laceration while cutting teeth from piglets (10). Interestingly, in this patient, there were no localized signs of infection noted.

Pasteurella aerogenes, found in the digestive tract of pigs, has often been isolated from human wounds associated with pig bites or exposure (10, 66, 147). Other organisms associated with human infections after a pig bite have included *Actinobacillus suis* (70), a *Flavobacterium* group IIb-like organism (95), and MRSA (51).

Recent studies, mostly from the Netherlands, have shown a high prevalence of nasal MRSA colonization in people commonly in contact with live pigs (133, 137, 203, 219, 226, 238). Molecular characterization of MRSA found in pigs and humans commonly in contact with pigs has revealed that the MRSA isolate often belonged to *Staphylococcus aureus* protein A (*spa*) type t108 and sequence type 398 (ST398) (137, 218, 224, 226). The clonal spread and transmission of *spa* type t108 and ST398 MRSA isolates among family members of a pig farmer, his coworkers, and his pigs have been reported (119).

Rabies virus infection of a pig has been reported (63). However, to our knowledge there has not been any reports of rabies virus transmission from pigs to humans.

Ferrets. Ferrets are kept by many as exotic pets. Young children and infants seem to be at the greatest risk for severe bites. In a study of the oral microflora of five ferrets at the gingival sulcus and mucosal membrane, commonly isolated bacteria belonged to *Pasteurella*, *Corynebacterium*, and *Rothia* species (74). No anaerobic bacteria were isolated from the cultures. Anaerobes, specifically *Porphyromonas gulae* and *Fusobacterium* species, were found in ferrets with ligature-induced periodontitis (74). Jones et al. (125) reported a case of recurrent *Mycobacterium bovis* infection following a ferret bite. Rabies may also be transmitted by ferret bite.

Horses. Humans and horses have shared a close relationship with one another over thousands of years. Throughout the world, millions of people have contact with horses through recreation or sporting or for occupational reasons. In 1958, Carithers reported that 5 out of 157 (3%) animal bites seen in children in Jacksonville, FL, over a 20-month period were

TABLE 6. Bacteria isolated from horse bite wounds in humans[a]

Bacterium isolated from horse bite wounds
Actinobacillus equuli-like bacterium
Actinobacillus lignieresii
Actinobacillus suis
Bacteroides fragilis
Campylobacter ureolyticus[b]
Escherichia coli
Neisseria species
Pasteurella caballi
Prevotella melaninogenica
Staphylococcus aureus
Streptococcus anginosus
Streptococcus mutans
Yersinia species

[a] Based on data from references 12, 59, 71, 156, 165, 177, and 180.
[b] Previously *Bacteroides ureolyticus*.

horse bites (30). In England, over a 2-year period, a local hospital reported 622 patients with horse-related injuries, 24 (3.8%) of which were bite wounds (65). In this case series, very few had extensive muscle damage, and most injuries healed uneventfully. In eastern Turkey, over a period of 2 years, horse bites accounted for 17% of animal bite injuries and were second only to dog bites (69%) (69). It has been estimated that roughly 3% to 4.5% of all horse-related injuries are from bites (143).

Most reports of the bacteriology of horse bite wounds in humans have revealed infections to be polymicrobial, with a mixture of aerobic and anaerobic organisms (59, 177). Table 6 lists the bacteria isolated from horse bite wounds in humans.

Actinobacillus lignieresii in infected wounds of humans bitten by horses has often been reported (12, 59, 177). *Actinobacillus* species, specifically *Actinobacillus suis*, has been found to be a part of normal horse oral and upper respiratory tract floras (16, 134). Peel et al. (177) reported two cases of *Actinobacillus* infections from a horse bite. For one patient who had an infected hand bite wound, the cultures grew *Actinobacillus lignieresii*, an *Actinobacillus equuli*-like bacterium, *Staphylococcus aureus*, and oral *Neisseria* and *Streptococcus* species. The wound cultures of the other patient, who sustained a bite and an open forearm fracture and who had repeated infections, grew *Actinobacillus suis*, *Staphylococcus aureus*, *Prevotella melaninogenica*, *Escherichia coli*, and *Pasteurella multocida*. The identification of *Actinobacillus lignieresii* can also be difficult, and this organism may be mistaken for a *Pasteurella pneumotropica* isolate (59, 146, 177). *Escherichia coli* and *Bacteroides* species have also been reported for infections with foul-smelling purulent drainage from horse bite wounds (59).

Other organisms isolated from human horse bite wounds have included *Streptococcus anginosus* and *Streptococcus mutans*, from an infected laceration (156); *Campylobacter ureolyticus*, *Prevotella melaninogenica*, and *Bacteroides fragilis*, from a purulent wound with a subsequent development of osteomyelitis (165); *Pasteurella caballi* (71); and *Yersinia* (180). Wound infection with *Staphylococcus hyicus* subsp. *hyicus* after a donkey bite was reported (173).

Sheep. *Actinobacillus lignieresii* has been recovered from a pure culture from an infected wound in a patient who sustained a bite injury from a sheep over his finger (177).

Tasmanian devils. Tasmanian devils are Australian marsupials. Georghiou et al. reported a case of a 5-year-old boy with a *Pasteurella multocida* infection following a Tasmanian devil bite (87).

Reptiles

Snakes. The true global incidence of human injuries inflicted by snake bites or envenomations and associated deaths is unknown (40, 128, 229). It was estimated that between 1.2 million and 5.5 million humans are bitten by snakes annually. Of these, at least 421,000 to 1,841,000 are envenomations and 20,000 to 94,000 lead to death (128). Most venomous snake bites occur in Southern and Southeastern Asia, sub-Saharan Africa, and Central and South America (128). In the United States, an estimated 7,000 venomous snake bites occur annually, with a mortality rate of less than 1% (see the Texas Department of State Health Services Zoonosis Control Branch website [http://www.dshs.state.tx.us/idcu/health/zoonosis/Animal/Bites/Information/venom/snake/]). Bites from nonnative venomous snakes, often involving cobras, have also been reported in the United States (159).

Investigations into the oral bacterial flora of various snakes and their venom have revealed a mixture of both aerobic and anaerobic bacterial species (94, 141, 201, 211). Studies of the oral flora bacteriology of Chinese cobras, bamboo pit vipers (201), and Malayan pit vipers (211) have yielded a plethora of aerobic and anaerobic organisms, such as coagulase-negative staphylococci, *Proteus* species, *Morganella morganii*, *Aeromonas hydrophila*, *Enterococcus faecalis*, and *Clostridium* species. Common bacterial isolates from venom of 15 captive rattlesnakes included *P. aeruginosa*, *Proteus* species, coagulase-negative staphylococci, *Clostridium* species, and *Bacteroides fragilis* (94).

Goldstein et al. studied the venom of four rattlesnakes with their fang sheaths retracted and decontaminated and found that 50% of the samples of the venom had no bacterial growth (94). It is likely that the isolated oral flora of rattlesnakes reflects the fecal flora of ingested prey. In addition, venom may also possess some antibacterial activity against some of the organisms isolated from snake oral flora (207, 211). In a study of venoms from three crotalid species, it was noted that the venom had some antibacterial activity against staphylococci, *Pseudomonas aeruginosa*, and *Enterobacter*, *Citrobacter*, *Proteus*, and *Morganella* species but not against anaerobic isolates (207). This potential antibacterial property of venom may have some antagonistic role in the overall pathogenesis of infection after envenomation injuries and may explain the observed low incidence of wound infection in snake bite victims (18, 44, 132, 150).

Polymicrobial infections are commonly observed for patients with infected wounds secondary to a snake bite (127, 131). Jorge et al. reported 40 patients with abscesses at the site of *Bothrops* bites, none of whom were previously treated with antimicrobials (127). Those authors found that *Morganella morganii* was the most frequently isolated organism (23 patients). Other organisms isolated, in order of decreasing frequency, included group D streptococcus, *Providencia rettgeri*, *Bacteroides* species, *Enterobacter* species, and *Escherichia coli*. A mixture of aerobic and anaerobic organisms with enteric,

coliform organisms accounted for the majority of isolates and was also observed for abscesses secondary to pit viper envenomation (131).

More recently, Garg et al., in a retrospective study, reported the bacteriology of 43 wound infections secondary to snake bite (86). Fifty-six percent of patients presented with a subcutaneous abscess, and the remainder had localized tissue necrosis. Interestingly, in that study, approximately 80% of the infections were monobacterial (likely due to a major limitation of the study in that anaerobic cultures were not performed). The most commonly found organisms isolated included *Staphylococcus aureus*, *Escherichia coli*, coagulase-negative staphylococcus, *Enterococcus faecalis*, and *Klebsiella pneumoniae*. Other organisms less frequently observed included *Proteus* species, *Morganella morganii*, *Pseudomonas aeruginosa*, *Acinetobacter* species, *Enterobacter* species, and *Streptococcus* species.

Human infections with *Mycobacterium ulcerans* (112), *Aeromonas jandaei* (196), *Enterobacter aerogenes* (formerly *Aerobacter aerogenes*) (149), *Serratia marcescens* (S. A. Minton and F. Russell, personal communication), *Clostridium perfringens* (123), and *Clostridium tetani* (204) following snake bites have been reported.

Komodo dragon. Komodo dragons are native of Komodo, Rinca, Flores, and Gili Motang in the Indonesian Islands and are the largest living lizards, reaching a length of approximately 10 feet and weighing 150 pounds. In addition, they are held in captivity in many zoos around the world. They are carnivores and eat mostly carrion but will prey on birds and mammals.

Montgomery et al. (162) took oral and saliva samples for aerobic cultures from 23 wild Komodo dragons in Komodo National Park, Indonesia, and from 13 captive animals at the Gembira Loka zoo in Yogyakarta, Java. Those authors reported that captive Komodo dragons had "significantly" fewer species isolated than did wild species. *Escherichia coli* was the most commonly found isolate, found in 39% (9 out of 23) of wild Komodo dragon mouths, while *Staphylococcus capitis* (5 out of 13 [38%]) and *Staphylococcus caseolyticus* (5 out of 13 [38%]) were the isolates most commonly found in captive Komodo dragon mouths. Table 7 lists the bacteria found in wild and captive Komodo dragons. *Pasteurella multocida* is not typically part of reptilian oral flora, and it is likely acquired transiently in Komodo dragons through the ingestion of prey animals (82).

A recent study by Citron et al. (43) reported the growth of 17 aerobes and 8 anaerobes from the mouths of two captive Komodo dragons. The male Komodo dragon had eight aerobic and three anaerobic species, while the female had nine and five, respectively. Both Komodo dragons grew 3+ to 4+ enteric bacilli, including *Escherichia coli*, *Klebsiella oxytoca*, *Enterobacter* species, and *Providencia rettgeri*. Both Komodo dragons had heavy growth of *Enterococcus faecalis*, and the female also had *Streptococcus dysgalactiae*. Both Komodo dragons had coagulase-negative *Staphylococcus* species, including *Staphylococcus sciuri*, and a variety of Gram-positive rods, including *Bacillus cereus*, *Rothia* species, and *Corynebacterium* species. The female Komodo dragon grew *Fusobacterium varium*, two other Gram-negative rods resembling *Bacteroides* and *Parabacteroides* species, *Clostridium perfringens*, and *Clostridium sardiniense*. The male grew *Bacteroides fragilis*, *Clostridium sordellii*,

TABLE 7. Oral bacteriology of wild and captive Komodo dragons

Organism	No. of isolates from Komodo dragon wounds determined by:		
	Montgomery et al.[a]		Citron et al.[b] for captive animals (n = 2)
	Wild (n = 23)	Captive (n = 13)	
Aerobic Gram-positive organisms			
Aerococcus species	2	0	
Bacillus cereus	3	0	2
Bacillus coagulans	1	0	
Bacillus stearothermophilus	1	0	
Bacillus subtilis	4	0	
Bacillus species	4	0	
Brevundimonas diminuta	2	0	
Corynebacterium species	7	0	2
Enterococcus faecalis	1	0	2
Enterococcus casseliflavus	1	0	
Kurthia species	0	2	
Micrococcus species	5	0	
Rothia species			2
Staphylococcus aureus	5	3	
Staphylococcus auricularis	1	0	
Staphylococcus capitis	0	5	
Staphylococcus caseolyticus	0	5	
Staphylococcus cohnii	0	1	
Staphylococcus gallinarum	1	0	
Staphylococcus haemolyticus	2	1	
Staphylococcus hominis	1	0	
Staphylococcus kloosii	1	0	
Staphylococcus saprophyticus	1	0	
Staphylococcus sciuri	2	0	2
Staphylococcus warneri	1	2	
Staphylococcus xylosus	1	1	
Staphylococcus species	10	0	
Streptococcus bovis	1	0	
Streptococcus agalactiae	1	0	
Streptococcus dysgalactiae			1
Streptococcus species	14	0	
Aerobic Gram-negative organisms			
Acinetobacter calcoaceticus	2	0	
Aeromonas hydrophila	2	1	
Alcaligenes faecalis	2	0	
Burkholderia cepacia	3	0	
Enterobacter species	6	3	2
Escherichia coli	9	1	2
Klebsiella species	9	1	2
Pasteurella multocida	2	0	
Proteus mirabilis	5	2	
Providencia rettgeri	1	0	2
Pseudomonas species	5	1	
Serratia species	4	1	
Anaerobic organisms			
Fusobacterium varium			1
Bacteroides fragilis			1
Bacteroides species			1
Parabacteroides species			1
Clostridium perfringens			1
Clostridium sardiniense			1
Clostridium sordellii			1
Swarming *Clostridium* species			1

[a] Based on data from reference 162.
[b] Based on data from reference 43.

and a swarming *Clostridium* species.

Komodo dragon attacks on humans are rare, with three having been reported in the press, but to our knowledge, there has not been any report of the bacteriology of infected human wounds from bites of this animal.

Monitor lizards. Monitor lizards, also known as biawak or goannas, belong to the genus *Varanus* and are related to Komodo dragons. A case of *Pseudomonas aeruginosa* septic arthritis after a bite from a monitor lizard was reported (210).

Iguana. Iguanas are popular exotic pets in the United States. In a recent report from poison centers in Texas between 1998 and 2008, 59 iguana bites were cited (79a). A majority of the injuries often involve the upper extremities (commonly fingers) and face (14, 79a). Data on the microbiology of infected human wounds from iguana bites are restricted to a few case reports (101, 117). An 8-year-old boy was bitten on his left index finger and developed purulent cellulitis that grew *Serratia marcescens* and *Staphylococcus aureus* (117). Two cases of *Serratia marcescens* bullous cellulitis in adults following iguana bites have also been reported (101). It is noteworthy that *Serratia* species is commonly resistant to aminopenicillins, an antibiotic class commonly prescribed for animal bites. It is often susceptible to fluoroquinolones, carbapenems, and aminoglycosides.

Alligators/crocodiles. Both the alligator population and human encounters with alligators have increased in the United States (142). The same situation exists for crocodiles in Australia (27, 103). From 1948 to 2004, there were 376 injuries and 15 deaths reported to be due to alligators in the United States (142). In 2009, 11 provoked and 8 unprovoked alligator attacks were reported in Florida (see the Florida Fish and Wildlife Conservation Commission website [http://myfwc.com/docs/WildlifeHabitats/Alligator_GatorBites.pdf]). Unprovoked bites were defined as bites on human beings from wild alligators, which were not provoked by handling or intentional harassment.

Flandry et al. (76) investigated the oral microbiology of 10 American alligators (*Alligator mississippiensis*) and found a plethora of aerobic and anaerobic bacteria, including *Aeromonas hydrophila*, in all 10 alligators. Other isolates found included *Citrobacter freundii*, *Klebsiella oxytoca*, *Pasteurella haemolytica*, *Pseudomonas pickettii*, *Bacteroides thetaiotaomicron*, *Bacteroides vulgatus*, other *Bacteroides* species, *Clostridium clostridioforme*, *Clostridium tetani*, *Fusobacterium nucleatum*, and *Peptostreptococcus* species.

Data on the microbiology of human wounds inflicted by alligators or crocodiles are limited to a few case reports (76, 228). In a report of a 22-year-old male with an infected thumb injury following an alligator bite, wound cultures grew *Aeromonas hydrophila*, *Enterobacter agglomerans*, *Citrobacter diversus*, *Enterococcus* species, and *Clostridium* species (76). Recently, Wamisho et al. (228) reviewed their experience with five Malawian patients bitten by crocodiles, in which one wound culture grew a *Citrobacter* species. In their review of the literature, they noted that other investigators isolated *Vibrio vulnificus*, *Citrobacter* species, *Burkholderia pseudomallei*, *Pantoea agglomerans*, *Bacteroides melaninogenicus*, *Aeromonas hydrophila*, *Serratia fanticola*, *Clostridium perfringens*, *Pseudomonas aeruginosa*, and *Proteus vulgaris*. Caiman bites in Brazil have been reported, and it was speculated that their oral flora might be similar to that of alligators in the United States (108).

Rodents

Rats. It is estimated that there are 20,000 rat bites in the United States annually. Children are commonly bite victims, as rats and other rodents have gained popularity as pets (68, 88). With respect to diseases associated with rats, most attention has been related to rat bite fever, an ancient disease caused by *Streptobacillus moniliformis*, a fastidious, highly pleomorphic, filamentous, Gram-negative rod, and *Spirillum minus*, a short, tightly coiled, Gram-negative rod (68). *Streptobacillus moniliformis* infection is more common in North America, while *Spirillum minus* is more common in Asia.

Ordog et al. conducted a prospective study of 50 patients with uninfected rat bite wounds (172). Bacterial isolates were cultured for only 30% of wounds, 43% of which were *Staphylococcus epidermidis* isolates and the remainders of which were *Bacillus subtilis*, alpha-hemolytic *Streptococcus*, and diphtheroid isolates. Prophylactic antibiotics were withheld, and only one patient developed infection. *Actinobacillus equuli* has been isolated from the nasopharynx of laboratory mice and rats (146). *Actinobacillus lignieresii* has also been isolated from the middle ear and nasopharynx of laboratory rats (146).

Cases of rat bite-associated infections of humans with *Corynebacterium kutscheri* (114) and *Leptospira* (98, 151) have been reported.

Guinea pigs. Guinea pigs are common household pets of children. *Actinobacillus equuli* has been isolated from the conjunctiva and posterior nasopharynx of laboratory guinea pigs (146). Case reports of *Haemophilus influenzae* (191) and *Pasteurella* species (148) infections after guinea pig bites have been published.

Hamsters. Tularemia in a 3-year-old boy following a hamster bite to his finger shortly before the hamster died has been reported (37). A left axillary lymph node biopsy specimen grew *Francisella tularensis*. A case of a glandular form of tularemia acquired during hamster hunting has been reported (160).

Prairie dogs. A case of a *Francisella tularensis* infection in a 3-year-old boy following a prairie dog bite was reported (2).

Birds

Human infections from bird bites are generally minor and rare, but a few case reports have been made. Berkowitz and Jacobs (13) reported a fatal case of a 16-month-old girl who was pecked on her head by a rooster and 4 days later presented with seizures. She died 6 days after admission, and her brain tissue grew *Streptococcus bovis*, *Clostridium tertium*, and *Aspergillus niger*. Those authors concluded that soil microorganisms contaminated by chicken feces were the most likely source of the organisms. Davis and Wenzel (50) reported a man attacked by a horned owl, who developed a scalp infection that grew two undetermined but different *Bacteroides* isolates.

Swans. A *Pseudomonas aeruginosa* infection in a 39-year-old woman who was vigorously pecked on a finger while feeding a swan was reported (64).

Sharks

The International Shark Attack File reported 455 shark attacks from 1999 to 2009 in the United States (http://www.flmnh.ufl.edu/fish/sharks/isaf/isaf.htm). The majority of attacks occurred in Florida (294 attacks), Hawaii (42 attacks), South Carolina (32 attacks), and California (30 attacks). Worldwide, during the same period, 700 shark attacks were reported, with 51 (7.3%) being fatal attacks. The highest numbers of attacks worldwide, in order of decreasing frequency, were reported from Florida, Australia, Hawaii, South Africa, and California.

Buck et al. (24) studied the oral aerobic flora of a male great white shark from Connecticut waters and recovered various isolates of *Vibrio* species, such as *Vibrio parahaemolyticus*, *Vibrio alginolyticus*, and *Vibrio fluvialis*. Other isolates included *Pseudomonas putrefaciens*, "gold-pigmented" *Staphylococcus* species, *Citrobacter* species, and *Micrococcus* species. *Vibrio carchariae*, initially mistaken for a *Clostridium* species, was isolated from an infected wound in a shark bite victim swimming off the South Carolina coast (176). Royle et al. (194) reported two cases of infections following shark bites in Australia. The wound cultures from one of the patients grew *Vibrio parahaemolyticus* and *Aeromonas caviae*, and the cultures from the other patient grew *Vibrio alginolyticus*, *Aeromonas hydrophila*, *Proteus* species, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Clostridium freundii*, and an *Enterococcus* species.

SUMMARY AND FUTURE DIRECTIONS

Our review has focused on infected dog and cat bite wounds in humans and a variety of more exotic animal bite wound infections. As noted above, the bacteriology of even common dog and cat bite wounds is diverse, and despite the use of currently optimal aerobic and anaerobic culture methods, approximately 7% of infected wounds still do not yield bacterial growth. This suggests that other more fastidious pathogens, including *Chlamydia*, mycoplasmas, and perhaps even viruses, may be involved in these wounds. Additional systematic studies of these wounds employing new molecular diagnostic techniques are needed. Another issue is the lack of an understanding of the pathogenic significance of all these cultured organisms. Perhaps antimicrobial treatment studies with a differing spectrum of activity may shed some light in this area. In addition, systematic studies with strict infection criteria are needed. A majority of the data have come from case reports with no established criteria for an infected wound. Organizing a research network among zoos, veterinary practices, and rural clinics and hospitals may be helpful in gathering information in a more methodical fashion. One can hope for future interest in and research on these issues, but to paraphrase Robert Frost, we have miles to go before we sleep.

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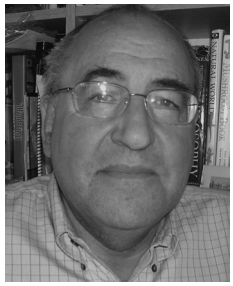

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