Wound Infection with *Neisseria weaveri* and a Novel Subspecies of *Pasteurella multocida* in a Child Who Sustained a Tiger Bite

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A 7-year-old girl developed a wound infection as a result of a tiger bite she sustained. DNA sequence analysis revealed that the causative organisms were *Neisseria weaveri* and what is, to our knowledge, a previously undescribed subspecies of *Pasteurella multocida*, for which we propose the designation "*Pasteurella multocida* subspecies *tigris* subspecies nov."

Tiger bites are an uncommon cause of wound infection in humans. As with bite wounds from domesticated cats [1], *Pasteurella multocida* has frequently been implicated, often as part of a polymicrobial infection [2–4]. We describe a child who developed a wound infection with *Neisseria weaveri* and a novel subspecies of *P. multocida* after an unfortunate encounter with an adult white Siberian tiger.

**Methods.** Bacteria were identified at the Mayo Clinic Clinical Microbiology Laboratory (Rochester, MN) according to accepted morphologic and biochemical (with tubed biochemicals) characteristics. Bacteria were additionally characterized by 16S rDNA sequence analysis using the MicroSeq 500-bp 16S rRNA bacterial sequencing kit (Applied Biosystems) in conjunction with data analysis using the MicroSeq software and GenBank. Full-length 16S rDNA PCR amplification and sequencing of the *Pasteurella* isolate was performed using cycling conditions and primers [5] and PCR mixtures described elsewhere [6]. The sequence data were analyzed using Sequencher 3.0 (Gene Codes). The 16S rDNA sequence of the 2 bacterial isolates (*N. weaveri* and *P. multocida* subspecies *tigris* subspecies nov.) have been deposited in GenBank under accession numbers AY057993 and AY057994, respectively. *P. multocida* subspecies *tigris* subspecies nov. has also been deposited in the American Type Culture Collection (accession number pending).

**Case report.** A 7-year-old girl presented to the emergency department at May Eugenio Litta Children’s Hospital (Rochester, MN) shortly after being bitten by an adult white Siberian tiger, which was described as being ∼225 kg in weight. The girl was visiting a local, privately owned animal reserve with her mother, when the tiger broke through a chain-link fence unprovoked and picked up the girl in the left shoulder region with its mouth. The girl was carried for ∼12 m before the tiger released her. Although fully conscious and oriented, she was bleeding from 2 bite wounds on her back, and she was transported by ambulance to the emergency department.

The child’s immunizations, including a recent tetanus toxoid booster, were up to date. At physical examination, she was alert and had normal vital signs. She had a 6-cm laceration over the left chest near the anterior axillary line and a 3-cm laceration over the left posterior scapula. The findings of further physical examination and laboratory studies were unremarkable. A chest radiograph revealed clear lung fields and no evidence of pneumothorax. Aerobic and anaerobic cultures of wound and blood samples were performed intraoperatively.

The girl underwent irrigation, debridement, and closure with surgical drains of both wounds. After undergoing the operation, she received ampicillin-sulbactam as initial empiric therapy. On the second day of hospitalization, she developed a transient fever (temperature, 38.3°C).

Cultures of wound samples obtained intraoperatively grew *N. weaveri* and an organism most closely related to *P. multocida*, both of which were susceptible to all antimicrobial agents tested. The *Pasteurella* species was identified as an aerobic, gram-negative bacillus; it was determined to be urease negative, nonmotile, indole positive, nitrate positive, oxidase positive, and ornithine decarboxylase positive; it exhibited acid production from glucose, ribose, and sorbitol, but not from xylose, maltose, lactose, mannitol, sucrose, dulcitol, trehalose, or arabinose. A total of 1536 bases of 16S rDNA were sequenced; the sequence was 98.4% identical (1342 of 1364 bp) to that of *P. multocida* subspecies *septica* (GenBank accession number AF294411), 99.1% identical (1351 of 1364 bp) to that of *P. multocida* subspecies *gallicida* (GenBank accession number AF294412), and 98.9% identical (1350 of 1364 bp) to that of *P. multocida* subs-
species *multocida* (GenBank accession number AF294410). On the basis of phylogenetic evidence (figure 1), we propose the name “*Pasteurella multocida* subspecies *tigris* subspecies nov.”

Throughout the patient’s hospital course, the wound closures remained clean, dry, and intact, although she had persistent complaints of pain with movement of her left upper extremity. The surgical drains in both wounds were removed on the second day of hospitalization, and the patient was discharged from the hospital on the third day while receiving amoxicillin-clavulanate potassium and oxycodone. She was not given rabies prophylaxis. Three days later, the tiger was euthanized, in accordance with public health recommendations and state law; it was found to be negative for rabies. The patient was seen at a follow-up visit 2 weeks after discharge from the hospital. The incisions were well healed, and she had complete range of motion in both arms without any pain on movement.

**Discussion.** Infections secondary to tiger bites often result in rapid onset of cellulitis marked by pain, erythema, swelling, acute lymphadenitis, leukocytosis, and low-grade fever [8]. Septic arthritis, tenosynovitis, osteomyelitis, meningitis, and severe spinal cord injury have also been described [2–4]. One report noted delayed development of neurologic symptoms due to a posttraumatic syrinx after a patient sustained a tiger bite to the neck [9].

*N. weaveri* (previously named “CDC group M-5”) is an aerobic gram-negative bacillus that has been associated with wound infections secondary to dog and cat bites [10]. Septicemia due to *N. weaveri* has also been reported after a dog bite [11]. *P. multocida* has been previously reported to commonly colonize the oral cavity of tigers and other cats [4]. The *Pasteurella* species isolated in culture of our patient’s wound is related to—but not identical to—*P. multocida* subspecies described elsewhere. The 16S ribosomal DNA sequence was different from that of *P. multocida* subspecies described elsewhere. On the basis of its phylogenetic relationship with other *Pasteurella* species and the source animal, we have proposed that the name *P. multocida* subspecies *tigris* subspecies nov. be applied to the organism we describe.

Of importance, it has been suggested that *P. multocida* subspecies *septica* might be more appropriately considered a separate species [12]. Further studies (e.g., studies based on DNA-DNA hybridization) are needed to clarify whether the relatively high sequence difference of *P. multocida* subspecies *tigris* subspecies nov. to *P. multocida* subspecies *gallicida* and *P. multocida* subspecies *multocida* would justify the classification of *P. multocida* subspecies *tigris* subspecies nov. as a separate species.

*Pasteurella* species should be considered a potential pathogen after any cat bite. In the case of a tiger bite, the possibility for involvement of deep structures should be considered, and thorough debridement and irrigation should be performed. Samples should be obtained intraoperatively for deep wound cultures, and the patient should receive empiric antimicrobial therapy. Polymicrobial infection, often with unusual organisms, should be anticipated, and ampicillin-sulbactam is recommended as initial empiric therapy. For patients with a β-lactam allergy, clindamycin plus trimethoprim-sulfamethoxazole is an appropriate alternative [13]. The need for tetanus prophylaxis and the risk for rabies infection should be assessed.

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**Figure 1.** Distance matrix tree derived from sequence homology determinations of 1377 base pairs of 16S ribosomal DNA. The tree was constructed using the neighbor-joining method [7]. The GenBank accession numbers of the 16S ribosomal DNA of the organisms are shown. The scale bar represents a 1% difference in nucleotide sequence, as determined by calculating the sum of all of the horizontal lines connecting 2 species.
References


