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Abstract: Bartonella species are emerging pathogens that have been isolated worldwide from humans and other mammals. Our objective was to estimate the prevalence of Bartonella infection in free-ranging African lions and cheetahs. Blood and/or serum samples were collected from a convenience sample of 113 lions and 74 cheetahs captured in Africa between 1982 and 2002. Whole blood samples available from 58 of the lions and 17 of the cheetahs were cultured for evidence of Bartonella spp., and whole blood from 73 of the 74 cheeths tested for the presence of Bartonella DNA by TagMan PCR. Serum samples from the 113 lions and 74 cheetahs were tested for the presence of antibodies against B.henselae using an immunofluorescence assay. Three (5.2%) of the 58 lions and one (5.9%) of the 17 cheetahs were bacteremic. Two lions were infected with B.henselae, based on PCR/RFLP of the citrate synthase gene. The third lion and the cheetah were infected with previoulsy unidentified Bartonella strains. Twenty-three percent of the 73 cheetahs tested by TagMan PCR were positive for Bartonella spp. Bartonella henselae antibody prevalence was 17% (19/113) for the lions and 31% (23/74) for the cheetahs. The prevalence of seropositivity, bacteremia, and positive TaqMan PCR was not significantly different between sexes and age categories (juvenile vs. adults) for both lion and cheetahs. Domestic cats are no longer the only known carriers of Bartonella spp. in Africa. Translocation of B.henselae seronegative wild felids might be effective in limiting the spread of Bartonella infection.

1 2 3	Prevalence of Bartonell	a infection in free-ranging African lions (Panthera leo) and cheetahs (Acinonyx jubatus)						
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## Abstract

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Bartonella species are emerging pathogens that have been isolated worldwide from 2 humans and other mammals. Our objective was to estimate the prevalence of Bartonella 3 infection in free-ranging African lions (Panthera leo) and cheetahs (Acinonyx jubatus). Blood 4 and/or serum samples were collected from a convenience sample of 113 lions and 74 cheetahs 5 captured in Africa between 1982 and 2002. Whole blood samples available from 58 of the 6 lions and 17 of the cheetahs were cultured for evidence of Bartonella spp., and whole blood 7 from 73 of the 74 cheetahs tested for the presence of Bartonella DNA by TaqMan PCR. 8 Serum samples from the 113 lions and 74 cheetahs were tested for the presence of antibodies 9 against B. henselae using an immunofluorescence assay. Three (5.2%) of the 58 lions and 10 one (5.9%) of the 17 cheetahs were bacteremic. Two lions were infected with B. henselae, 11 based on PCR/RFLP of the citrate synthase gene. The third lion and the cheetah were 12 infected with previously unidentified Bartonella strains. Twenty-three percent of the 73 13 cheetahs tested by TaqMan PCR were positive for Bartonella spp. Bartonella henselae 14 antibody prevalence was 17% (19/113) for the lions and 31% (23/74) for the cheetahs. The 15 prevalence of seropositivity, bacteremia, and positive TaqMan PCR was not significantly 16 different between sexes and age categories (juvenile vs. adult) for both lions and cheetahs. 17 Domestic cats are no longer the only known carriers of Bartonella spp. in Africa. 18 Translocation of B. henselae seronegative wild felids might be effective in limiting the spread 19 of Bartonella infection. 20

21 Key words: Bartonella, cheetahs, lions, serosurvey

#### 1. Introduction

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Members of the genus Bartonella are aerobic gram-negative bacteria that have recently been recognized as emerging pathogens (Anderson and Neuman, 1997). An increasing number of species have been described in the last decade and the genus currently consists of 16 species, seven of which are associated with human diseases (Jacomo et al., 2002). Clinical manifestations caused by Bartonella species include Carrion's disease, trench fever, cat scratch disease, bacillary angiomatosis, hepatic peliosis, endocarditis, chronic bacteremia, and neuroretinitis (Jacomo et al., 2002). The epidemiology of Bartonella infection is currently not fully understood but most Bartonella species are believed to be hosted by animal reservoirs and transmitted by arthropod vectors. Sand flies of the genus Lutzomyia are responsible for the transmission of B. bacilliformis (Garcia-Caceres and Garcia, 1991). The human body louse (Pediculus humanus) is the main vector for B. quintana (Maurin and Raoult, 1996). Cat fleas (Ctenocephalides felis) have been shown to transmit B. henselae between cats (Chomel et al., 1996), and various species of Bartonella have been identified in ticks (Schouls et al., 1999; Chang et al., 2001; Sanogo et al., 2003). Cat scratch disease (CSD) is the most common of the Bartonella-associated clinical conditions in humans and is estimated to have an incidence of 22,000 cases per year in the United States, representing an annual health care cost of more than \$ 12 million (Jackson et al., 1993). The main etiologic agent of CSD is Bartonella henselae (Regnery et al., 1992c; Dolan et al., 1993), which was first identified as the agent of bacillary angiomatosis in immuno-compromised patients (Regnery al., 1992a; Welch et al., 1992). Bartonella clarridgeiae has also been involved in the etiology of CSD based on serology results (Kordick et al., 1997; Margileth and Baehren, 1998).

Substantial evidence has accumulated identifying the domestic cat (Felis catus) as the 1 main reservoir for B. henselae. Natural and experimental infections of cats with B. henselae 2 were documented shortly after the bacterium was first identified (Regnery et al., 1992a; 3 Koehler et al., 1994; Abbott et al., 1997). No major clinical signs have been reported in cats 4 5 under natural conditions, although fever, transient anorexia, mild neurologic signs, myalgia, lymphadenopathy, and reproductive failure have been described in experimentally infected 6 7 cats (Breitschwerdt and Kordick, 1995; Greene et al., 1996; Guptill et al., 1997; Kordick and Breitschwerdt, 1997; Guptill et al., 1998; O'Reilly et al., 1999). Infected cats have been 8 shown to remain bacteremic for several months (Kordick et al., 1995; Abbott et al., 1997). 9 High B. henselae infection prevalence rates reported in cat populations (Koehler et al., 1994; 10 11 Chomel et al., 1995; Branley et al., 1996; Bergmans et al., 1997; Heller et al., 1997; Chomel 12 et al., 1999; Marston et al., 1999; Chomel et al., 2002), with a range of 16.5% to 61% depending on the origin of the cats tested, have later confirmed the reservoir role of cats. Cats 13 14 have subsequently been reported to be reservoir for B. clarridgeiae (Kordick et al., 1997) and B. koehlerae (Droz et al., 1999; Yamamoto et al., 2002), and have been shown to host B. 15 16 weissii (Regnery et al., 2000), which is now known as B. bovis (Bermond et al., 2002). Free-ranging felid species may likely be reservoirs for Bartonella species, as many 17 18 free-ranging felids of North America have been shown to be infected with Bartonella spp. 19 based both on serological and bacteriological data (Chomel et al., unpublished data). In 20 California, 26 (35%) of 74 mountain lions (Puma concolor) and 33 (53%) of 62 bobcats 21 (Lynx rufus) had antibodies against B. henselae in their blood (Yamamoto et al., 1998). In 22 Florida, antibodies against B. henselae were detected in two (28%) of seven mountain lions 23 originating from Texas (Puma concolor stanleyana), and in five (18%) of 28 Florida panthers

(Puma concolor corvi) (Rotstein et al., 2000). Statistical testing of the association between age and seropositivity showed that antibody prevalence was significantly higher in animals less than two years old than in animals over two years old (Rotstein et al., 2000; Yamamoto et al., 1998). Less clear is the association between sex and seropositivity. Yamamoto et al. (1998) found that male mountain lions were more likely to be seropositive than females. whereas Rotstein et al. (2000) found no significant difference in seropositivity status between males and females. Culture isolation and PCR-based speciation of the Bartonella strains were not performed in these two studies, and it is not known whether the Bartonella strains present in wild felids are the same as those in domestic cats.

Some evidence suggests that African free-ranging felid populations could be infected with Bartonella species. Infection of domestic cat populations with B. henselae has been documented in South Africa (Kelly et al., 1996; Pretorius et al., 1999). Kelly et al. (1998) isolated B. henselae from the blood of one of three cheetahs tested in Zimbabwe, and antibodies to B. henselae have been found in seven species of African wild felids (genera Acinonyx, Panthera and Felis) kept in different zoological parks of California (Yamamoto et al., 1998). Estimating the prevalence of Bartonella infection in African free-ranging felids is of interest to determine if wild felid populations could play a reservoir role for Bartonella species and could potentially serve as a source of infection for domestic cats and humans. Lions and cheetahs represent good candidate species for estimating the prevalence of infection in sub-Saharan African felids because they are widespread. The objectives of this study were 1) to estimate the prevalence of Bartonella infection in African lions and cheetahs by culturing blood samples for evidence of bacteria and by testing sera for the presence of antibodies against B. henselae using an immunofluorescence assay (IFA), 2) to identify the

- 1 Bartonella strains obtained, and 3) to test for association between Bartonella infection and
- 2 putative risk factors, including age, sex, and geographic location.

#### 2. Materials and methods

4 2.1. Animals

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5 Blood and serum samples were collected from 74 free-ranging cheetahs and 113 free-

6 ranging lions in Africa between September 1982 and February 2002. Fifty-eight lions had

serum and blood samples available and the other 55 lions only had serum samples available.

Whole blood was not available from one of the 74 cheetahs. The samples were obtained from

animals immobilized for disease surveillance or conservation purposes in Kruger National

Park in South Africa (112 lions), Masai Mara National Park (1 cheetah) and Nairobi National

Park (6 cheetahs) in Kenya, Ngorongoro crater (2 cheetahs) and Serengeti National Park in

Tanzania (1 lion, 13 cheetahs), and various regions of Namibia (52 cheetahs). Blood and

serum samples were stored at least at -20°C until tested.

#### 2.2. Blood culture

Whenever available, whole blood samples collected in EDTA tubes were centrifuged at 5000 x g for 30 min at room temperature. Blood pellets were resuspended in 125 µl of M 199 inoculation medium (Kohler et al., 1992) and plated onto heart infusion agar (Difco laboratories, Detroit, MI) containing 5% fresh rabbit blood. The plates were then incubated at 35°C in 5% CO<sub>2</sub> for four weeks, and cultures were examined at least twice weekly for bacterial growth. The number of colonies observed was recorded as the number of colony-forming units per milliliter of blood. Colonies were sub-cultured, harvested, and frozen at -70°C in M 199 inoculation medium containing 10% DMSO (Fisher Scientific, Fair Lawn, NJ). Identification of the isolates as Bartonella spp. was based on the phenotypic

- 1 characteristics of the colonies, and species determination was performed by polymerase chain
- 2 reaction-restriction fragment length polymorphism (PCR-RFLP) analysis of fragments of the
- 3 citrate synthase gene.
- 4 2.3. DNA extraction and PCR-RFLP analysis
- 5 Bacterial DNA was extracted from blood isolates by hot water extraction (15 min at 6 100°C). The extracted DNA was then used as a template for amplification of fragments of the 7 citrate synthase gene (gltA). Approximately 380 basepairs (bp) of the gltA gene were 8 amplified using previously described primers and methods (Norman et al., 1995). The 9 amplified products were verified by gel electrophoresis and then enzymatically digested 10 overnight, at 65°C using TaqI restriction endonuclease, and at 37°C using HhaI, MseI, and 11 Acil restriction endonucleases. Control samples included DNA from a strain isolated from a 12 naturally infected cat, which was previously confirmed positive for B. henselae, and a sample 13 with no DNA template. The digested fragments were separated by electrophoresis in a 3% 14 Nusieve GTG agarose gel (Biowhittaker Molecular Applications, Rockland, ME). Fragment 15 sizes were estimated by comparison with a 100-bp ladder (Invitrogen, Carlsbad, CA). Banding patterns were compared with those of other strains in the American Type Culture 16 17 Collection and our laboratory.
- 18 2.4. TaqMan PCR

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Blood samples collected in 1985, 1992, and 1993 from 56 cheetahs were too contaminated with fast-growing bacteria to allow for the culture of <u>Bartonella</u> spp., and were therefore tested by a <u>Bartonella</u> real-time TaqMan PCR system. In order to be consistent in our methodology, the 17 blood samples tested by blood culture were also submitted to TaqMan PCR testing. The real-time TaqMan PCR method is based on a combination of the

- 1 TaqMan technology and the ABI PRISM 7700 (Applied Biosystems, Foster City, CA) real-
- 2 time sequence detection system. The use of two specific primers and an internal labeled
- 3 TaqMan probe combined with the 5'-3' nuclease activity of Taq DNA polymerase allows
- 4 direct quantification of the PCR product accumulation during the exponential amplification
- 5 phase of the PCR. Quantification of the number of organism present in each sample is
- 6 obtained by using the standard curve method. Standard curves are optimized for the proposed
- 7 pathogens. The PCR mastermix contains a hot start enzyme (AmpliTaq Gold), an internal
- 8 dye (ROX) to normalize variations caused by manual pipetting and an AmpErase UNG
- 9 nuclease system to prevent PCR product carryover. Data collection and processing is
- 10 performed in an attached computer using ABI Sequence Detection System software.
- 11 2.4.1. Sample preparation for TaqMan PCR
- 12 One hundred μl of whole anticoagulated blood was used to extract genomic DNA (gDNA)
- 13 using DNeasy Tissue Kit (Qiagen, Valencia, CA). Briefly, whole blood was mixed with
- 14 proteinase K, PBS and lysis buffer AL to a final volume of 420 μl and digested for 10 min at
- 15 70°C. DNA was extracted according to the manufacturer's instruction.
- 16 2.4.2. TaqMan PCR systems
- 17 Two TaqMan PCR systems were used: first, a TaqMan PCR system specific for feline
- 18 glyceraldehyde-3-phosphate dehydrogenase (GAPDH, Leutenegger et al., 1999) was used as a
- 19 quality control to test for the integrity of the gDNA extracted from the aged blood samples.
- 20 In addition, a Bartonella specific TaqMan PCR system for detection of Bartonella spp. at the
- 21 genus level was used targeting the citrate synthase gene: forward primer Bart.738f: 5'-
- 22 GTGCTAATCCATTTGCATGTATT-3', reverse primer Bart.831r: 5'-

- 1 GTAACATTTTTAGGCATGCTTCATTA-3', TaqMan probe: Bart.772p: 5'-6-FAM-
- 2 AGCTGGTCCCCAAAGGCATGCAA-TAMRA-3'.
- 3 2.5. Serology

4 Sera from lions and cheetahs were tested by immunofluorescence assay (IFA) for the presence of antibodies against B. henselae. For antigen preparation, a B. henselae strain "U-5 4" (University of California, Davis) originally isolated from a naturally infected cat was 6 cultivated on Vero cells. Infected Vero cells were then suspended in L15/MEM tissue culture 7 medium (Invitrogen, Carlsbad, CA). Forty ul of the suspension were dotted onto each well of 8 12-well polytetrafluoroethylene-coated slides (Cel-line Associated, Newfield, NJ), and 9 incubated for 24 hours. The slides were then washed twice in phosphate-buffered saline 10 11 (PBS, pH 7.4, SIGMA, St Louis, MO), fixed 20 min in acetone, air dried, and then stored at -20°C. Sera from lions and cheetahs were diluted 1:64 in PBS containing 5% skim milk, and 12 then 20 µl of the 1:64 dilutions were added to the test wells of the slides. Positive and 13 negative control sera from domestic cats were included on all slides. Slides coated with test 14 sera were incubated 30 min at 37°C and then washed three times in PBS. Fluorescein-15 16 conjugated goat anti-cat immunoglobulin (whole-molecule immunoglobulin G; Cappel, Organon Teknika Corp., Durham, NC) was diluted 1:800 in PBS containing 5% skim milk 17 18 and 0.001% Evan's blue, and 20 µl of the mix were applied to each well. The slides were incubated 30 min at 37°C and then washed three times in PBS. Three µl of glycerol were 19 20 applied to each well and the slides then covered with a cover slip prior to interpretation with a fluorescence microscope (magnification x 400). The intensity of bacillus-specific 21 22 fluorescence was scored subjectively from one to four, and a fluorescence score greater than 23 two at a dilution of 1:64 was considered to be a positive result (Childs et al., 1994). A

- 1 double-blinded reading of each slide was performed by the same two readers. All serum
- 2 samples positive at 1:64 dilution were two-fold serially diluted and tested with the same IFA
- 3 technique to obtain an endpoint titer.
- 4 2.6. Statistical analysis
- 5 Statistical analyses were performed using Epi Info 2000 version 1.1.2 (CDC, Atlanta,
- 6 GA) and SPSS version 11.0 (SPSS Inc., Chicago, IL). Nonparametric tests (Chi-square,
- 7 Fisher's exact test) were used to test for an association between bacteremia or seropositivity.
- 8 and putative risk factors such as sex, age, and geographic origin of the animals. The
- 9 association between bacteremia and seropositivity was evaluated by paired analysis using the
- 10 McNemar Chi-square test.
- 11 3. Results
- 12 3.1. Description of the lion and cheetah populations
- One hundred and thirteen lions were included in the study. A precise age estimate was
- 14 available for 34 (30.1%) of them, ranging from 14 months to 15 years old (mean 69.9 months.
- 15 standard deviation 33.8 months). The age status was only known as juvenile (≤ 24 months
- old) or adult (> 24 months old) for 78 (69.0%) lions, and was undetermined for one (0.9%)
- 17 lion. Sixty-three (55.8%) lions were female, 49 (43.4%) were male, and the sex of one (0.9%)
- 18 lion was not recorded. Seventy-four cheetahs were included in the study and a precise age
- 19 estimate was available for 64 (86.5%) of them, ranging from six months to 16 years old (mean
- 20 42.9 months, standard deviation 35.1 months). The age status was only known as juvenile (≤
- 21 24 months old) or adult (> 24 months old) for six cheetahs, and was undetermined for four
- 22 cheetahs. Thirty-six (48.6%) cheetahs were female, 34 (45.9%) were male, and the sex of
- 23 four (5.4%) cheetahs was not recorded.

#### 3.2. Blood culture

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- 2 Bartonella were isolated from the blood of three (5.2%) of the 58 lions for which
- 3 whole blood samples were available. Bacteria of the genus Bartonella were isolated from the
- 4 blood of one (5.9%) of the 17 cheetahs for which non-contaminated blood samples were
- 5 available. The prevalence of bacteremic lions was not significantly different between males
- 6 (5.0% or 1/20) and females (5.3% or 2/38) or between juveniles (8.3% or 1/12) and adults
- 7 (4.3% or 2/46).
- 8 3.3. DNA extraction and PCR-RFLP analysis
- 9 Bartonella henselae was isolated from the blood of two of the bacteremic lions, and a
- 10 previously unidentified Bartonella strain, temporarily named "Lion 98-215", was isolated
- from the blood of the third bacteremic lion (Table 1). The three bacteremic lions were from
- 12 different locations in the Kruger National Park in South Africa (Table 1). The Bartonella
- 13 strain isolated from the blood of the bacteremic cheetah from Gobagos province in Namibia
- was also a previously unidentified strain temporarily designated as "Cheetah 1178".
- 15 3.4. TaqMan PCR
- Seventeen (23.3%) of the 73 cheetahs tested by TagMan PCR had a positive result.
- 17 The prevalence of positive TaqMan PCR result was not significantly different between males
- 18 (20.6% or 7/34) and females (22.9% or 8/35), between juveniles (32.1% or 9/28) and adults
- 19 (14.6% or 6/41), or between cheetahs from eastern Africa (28.6% or 6/21, of which 2/7 for
- 20 Kenya and 4/14 for Tanzania) and Namibia (21.2% or 11/52).
- 21 3.5. Serology
- 22 Antibodies against B, henselae were found in 19 (16.8%) of the 113 lions and in 23
- 23 (31.1%) of the 74 cheetahs. The prevalence of B. henselae seropositive lions was not

significantly different between males (12.2% or 6/49) and females (20.6% or 13/63) or 1 between juveniles (3.8% or 1/25) and adults (20.9% or 18/86). The prevalence of B. henselae 2 3 seropositive cheetahs was not significantly different between males (29.4% or 10/34) and females (33.3% or 12/36), between juveniles (25% or 7/28) and adults (35.7% or 15/42), or 4 5 between cheetahs from eastern Africa (45.5% or 10/22, of which Kenya 1/7 and Tanzania 9/15) and Namibia (25% or 13/52). Titers of serum antibodies against B. henselae ranged 6 7 between 1:64 and 1:1024 in both lions and cheetahs. No antibodies against B. henselae were 8 detected in one of the two lions found to be bacteremic with B. henselae. No antibodies 9 against B. henselae were detected in the lion found to be bacteremic with the Bartonella strain 10 "Lion 98-215", or in the cheetah found to be bacteremic with the Bartonella strain "Cheetah 11 1178" (Table 1). A summary of the culture, TaqMan PCR, and serology results is provided in 12 Table 2.

# 13 3.6. Paired analysis

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No significant association was detected between positive IFA and positive blood culture for the lions' samples. No association was detected between positive IFA and positive blood culture, or between positive IFA and positive TaqMan PCR for the cheetahs' samples. For the animals tested by both IFA and culture (58 lions and 17 cheetahs), 96.2% of the seronegative lions and 92.9% of the seronegative cheetahs were abacteremic. For the 73 cheetahs tested by both IFA and TaqMan PCR, 76% of the seronegative cheetahs had a negative TaqMan PCR result.

## 4. Discussion

This study reports the first isolation of <u>Bartonella</u> species from free-ranging African lions and the first prevalence estimate of <u>Bartonella</u> infection in free-ranging African lions

and cheetahs. <u>Bartonella henselae</u> seroprevalence detected here for lions (16.8%) and cheetahs (31.1%) are in the range of those reported in previous studies for North American free-ranging felids. Rotstein et al. (2000) found a seroprevalence of 18% in Florida panthers and 28% in mountain lions from Texas. In California, Yamamoto et al. (1998) reported a seroprevalence of 35% in mountain lions and 53% in bobcats. Unlike these two studies where juvenile animals had higher seropositivity prevalence than adults, but as observed in some reports for domestic cats (Haimerl et al. 1999; Gurfield et al., 2001), seropositivity prevalence was not significantly different between juvenile and adult lions or cheetahs. Similar to the study in Florida (Rotstein et al. 2000), but unlike the study in California (Yamamoto et al., 1998) where male mountain lions were more likely to be seropositive than females, antibody prevalence was evenly distributed between sexes for both African lions and cheetahs.

The prevalence of <u>Bartonella</u> positive blood culture in lions (5.2%) and cheetahs (5.9%) were low compared to those reported in previous studies of domestic and stray cats (Koehler et al., 1994; Chomel et al., 1995; Branley et al., 1996; Bergmans et al., 1997; Heller et al., 1997; Chomel et al., 1999; Marston et al., 1999; Chomel et al., 2002). Kelly et al. (1998) recently reported the isolation of <u>B. henselae</u> from one of three cheetahs tested in Zimbabwe. The low prevalence of positive blood culture in free-ranging cheetahs contrasts with the higher prevalence of positive TaqMan PCR results (23.3%). <u>Bartonella</u> are fastidious slow-growing organisms, and neither serology nor PCR methods have been shown to be more sensitive than culture to detect <u>Bartonella</u> infection in humans (La Scola and Raoult, 1999). It is therefore possible that the true bacteremia prevalence in our sample of wild cheetahs may be more accurately estimated by TaqMan PCR than by blood culture.

No serum antibodies against <u>Bartonella</u> were detected for the bacteremic cheetah and for two of the three bacteremic lions. Isolation of <u>Bartonella</u> from seronegative cats has previously been reported (Chomel et al., 1995; Kordick et al., 1995; Pretorius et al., 1999; Gurfield et al., 2001). Possible reasons for the absence of serological response include immunosuppression (especially in case of feline immunodeficiency virus (FIV) co-infection), collection of sera at an early stage of infection, or lack of antibody cross-reaction among strains.

The prevalence estimates reported here should be handled with precautions because of the limitations of the sampling scheme. The sample size was low and it could not be determined how representative our sample was of the free-ranging African lion and cheetah populations. These limitations, which are frequently encountered in studies of wildlife diseases, should be taken into account when readers make use of the results reported here.

Characterization of the two previously unidentified <u>Bartonella</u> strains, "Lion 98-215" and "Cheetah 1178", is currently in progress.

The existence of <u>Bartonella</u> infection in free-ranging felids of Africa has implications for public health. Transmission of CSD from cats to humans mainly occurs through scratches and bites. Flea-borne transmission has been suspected in humans and recent evidence of the presence of <u>B. henselae</u> in ticks suggests the possible existence of an arthropod vector (Sanogo et al., 2003). The arthropod-based transmission of <u>Bartonella</u> species from free-ranging felids to humans and domestic cats could occur when the large cats roam around human settlements to prey on livestock and small ruminants, or when people have access to national parks and other wildlife sanctuaries.

Seventy percent of the worldwide HIV cases are reported in Africa (De Cock et al., 2002) and Bartonella infection is likely to be a common secondary infection. Bacillary 2 3 angiomatosis, a severe manifestation of Bartonella infection, has previously been reported in different countries of southern Africa (Pretorius et al. 1999). Frean et al. (2002) recently 4 5 reported that 10% of 188 HIV-positive outpatients in Johannesburg, South Africa, were Bartonella bacteremic, as determined by nested PCR.

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The existence of Bartonella infection in free-ranging African felids also has implications in wildlife conservation because health data are indispensable for efficient population management. Further study should be done to investigate the clinical significance of Bartonella infection in African lions and cheetahs, and the possible effects of co-infection with other pathogens such as FIV. Bartonella henselae has been shown to contribute to chronic disease manifestations in domestic cats (Breitschwerdt and Kordick, 1995; Greene et al., 1996; Guptill et al., 1997; Kordick and Breitschwerdt, 1997; Guptill et al., 1998; O'Reilly et al., 1999), and could similarly affect wild felids.

Translocation of free-ranging felids can be a useful tool to reduce conflicts with expanding human populations, to repopulate protected areas in which animals have been decimated by poaching, and to maintain genetic diversity in metapopulations (Nowell and Jackson, 1996). Special care must be given to ensure that potential pathogenic agents are clearly identified and are not introduced into populations where they could have harmful effects. The existence of Bartonella infection should be taken into account prior to relocating lions and cheetahs. We reported that a negative serology result was highly predictive of a negative blood culture (96.2% in lions and 92.9% in cheetahs), and predictive of a negative TaqMan PCR (76% in cheetahs). Translocation of B. henselae seronegative wild felids might

- 1 therefore be effective in limiting the translocation of Bartonella species together with their
- 2 hosts.

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Table 1

Characteristics of <u>Bartonella</u> bacteremic animals out of 58 African free-ranging lions and 17

African free-ranging cheetahs tested for evidence of <u>Bartonella</u> by culturing whole blood samples

Species	ID	Sex	Age	Place of capture	Blood	Strain isolated	Bartonella
					culture		henselae
					(CFU/ml <sup>c</sup> )		antibody
							titer
Lion	98-215	M	Juvª	Undetermined (KNP <sup>b</sup> )	2000	<u>B</u> . "Lion 98-215"	0
Lion	150.41	F	6 y	Gomondwane (KNP)	93	B. henselae	0
Lion	7069	F	3.5 y	Nkulumbeni (KNP)	35	B. henselae	1:128
Cheetah	1178	M	7 y	Gobagos province	49	<u>B</u> . "Cheetah 1178"	0
				(Namibia)			

<sup>&</sup>lt;sup>a</sup> Juvenile (≤ 24 months old)

<sup>&</sup>lt;sup>b</sup> Kruger National Park, South Africa

<sup>&</sup>lt;sup>c</sup> Colony forming unit / ml of blood

Table 2

Prevalence of <u>Bartonella</u> infection in a convenience sample of 113 African free-ranging lions and 74 African free-ranging cheetahs tested by blood culture, TaqMan PCR and antibody immunofluorescence assay

Number of Bartonella	Number of animals with	Number of Bartonella	
bacteremic animals/ number	Bartonella DNA in their	henselae seropositive	
tested (%)	blood/ number tested (%)	animals/ number tested (%)	
3/58 (5.2%)	$ND^a$	19/113 (16.8%)	
1/17 (5.9%)	17/73 (23.3%)	23/74 (31.1%)	
	bacteremic animals/ number tested (%)  3/58 (5.2%)	bacteremic animals/ number Bartonella DNA in their tested (%) blood/ number tested (%)  3/58 (5.2%) ND <sup>a</sup>	

a Not done