Title: Exposure to bat-borne and other *Bartonella* species in humans in Ghana

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The research for this manuscript was carried out during fieldwork in southern Ghana; at the 37 Military Hospital in Accra; at the University of Cambridge, UK; and at the Centers for Disease Control and Prevention, Fort Collins, Colorado, USA.

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Summary line:

We report <1% prevalence of *Bartonella* antibodies among healthy people in Ghana.

Running title:

Bat-borne *Bartonella* Infections

Abstract (50 words)

This study reports < 1% prevalence of antibodies to common *Bartonella* species in healthy people in contact with bats in Ghana, and no exposure to a novel bat-borne *Bartonella* strain. One human
sample tested positive on PCR for *B. clarridgeiae* DNA. Among 70 domestic animals that lived underneath *E. helvum* roosting areas, one cat was positive for *B. henselae* DNA.

**Letter** (800 words)

Contact with wildlife is a leading cause of disease spillover. Bats in particular host numerous zoonotic pathogens, from henipaviruses to lyssaviruses (1). In Ghana, the straw-colored fruit bat (*Eidolon helvum*) frequently and closely interacts with people through urban roosting and bushmeat harvesting. Large colonies live in Accra, the capital city, and over 128,000 bats on average are hunted for food yearly from southern Ghana alone (2). Serological evidence of human infection with novel paramyxoviruses from *E. helvum* (3) supports concerns regarding this contact. Furthermore, Kosoy et al. (4) isolated several new strains of *Bartonella* present in over 30% of *E. helvum* and 66% of their ectoparasites, with unknown transmissibility to other species. This is concerning, as many *Bartonella* species are zoonotic and cause significant human disease (5).

Previous studies in febrile patients have shown up to 25% prevalence rates of antibodies to common *Bartonella* species in Thailand (6), but few studies have examined the general population and even fewer have been conducted in Africa (7). To address these concerns, we conducted a prevalence study in Ghana, West Africa for both bat-borne and common *Bartonella* species. We sampled both humans in close contact with fruit bats, as well as domestic animals around the bat colonies.

We sampled 335 Ghanaian volunteers with close contact with *E. helvum* from Accra and the Volta region, as well as 70 domestic animals living underneath bat colonies (5 cats, 23 chickens, 7 cows, 6 dogs, 21 goats, 8 sheep) from Accra. We used three testing approaches: culture, PCR, and indirect immunofluorescent assays (IFA) for serology. We tested sera for antibodies against *B. henselae, B. quintana, B. clarridgeiae, B. vinsonii vinsonii, B. elizabethae*, and the strain E1-105 isolated from *E. helvum* (5).
All human and domestic animal culture results were negative for *Bartonella* species. One human
serum sample was positive for *B. clarridgeiae* using PCR, confirmed on repeat testing. There were
no other consistently positive human samples on PCR. Of 70 animal blood clots and 62 sera
samples tested using PCR, one serum sample from a cat tested positive for *B. henselae*. One human
serum sample was positive for antibodies on IFA against *B. henselae* at 1:128, another had
reactivity to *B. henselae* at 1:64 and one at 1:32. Five human serum samples were reactive to *B.
quintana* at 1:32.

The absence of any human exposure to bat-borne *Bartonella* suggests that the species isolated from
*E. helvum* is either never or rarely infects human beings in Ghana. If *Nycteribiidae* bat flies serve as
the vector for *Bartonella* transmission between bats as hypothesized, then the high host specificity
of these vectors (8) could explain why little infection is spilling over to other species. However, no
experimental studies have confirmed that bat flies are competent vectors of bat-borne *Bartonella*
species or that these ectoparasites only bite bats. These facts are important to confirm, as bat flies
are occasionally found on other animals—whether the parasites can successfully use these animals
as hosts is unknown (8). While further studies are needed to understand the dynamics of *Bartonella*
species infection in *E. helvum*, as well as its zoonotic potential, the current risk of spillover of this
bat-borne *Bartonella* species appears low in West Africa. This fact may be useful in directing
limited public health resources.

The seroprevalence to *B. henselae* in healthy human subjects in this study was <1%. The low levels
of seropositivity to *B. henselae* and *B. quintana* is consistent with the only other study on
*Bartonella* in human beings in sub-Saharan Africa; a survey of 155 subjects in the Democratic
Republic of Congo showed a 1% seroprevalence of *B. henselae* and < 1% of *B. quintana* (8).
Both the Congolese study and this study contrast with some studies in Asia and Europe, which show higher rates of exposure to both *B. henselae* and *B. quintana*. For example, a study of Thai febrile patients found serological evidence of *Bartonella* infections in 25% of subjects (7).

Laudisoit et al. (8) were first to report evidence of *Bartonella* infection in human beings in Africa. Our study contributes to this nascent effort of understanding *Bartonella* on the continent. As a substantial proportion of *Bartonella* prevalence studies have been done on hospital patients, our study provides an important general population survey to help determine background infection rates and to illuminate the complex risks posed by this zoonosis.
REFERENCES


