

Q fever epidemic in Cayenne, French Guiana, epidemiologically linked to three-toed sloth

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ABSTRACT

A Q fever epidemic occurred in 2013 in a small military residential area in Cayenne, French Guiana. A retrospective cohort study was conducted to identify Q fever risk factors. Confirmed acute Q fever case was defined as positive serology (IgM $\geq$ 50 and phase II IgG $\geq$ 200) and/or positive qPCR on serum or blood. In addition, wild mammals were captured at the study site and tested by serology and real-time PCR performed on blood, vaginal swabs and ticks. The attack rate was 20 percent (11/54). All the cases were symptomatic with fever $> 38.5^\circ\text{C}$ and community-acquired pneumonia for four cases. Log binomial multivariate models identified two independent risk factors associated with Q fever: to clean the house (RRa = 7.5 CI95% [1.03–55.3]) and to carry a three-toed sloth in arms (RRa = 2.6 CI95% [1.1–5.8]). Eighteen marsupial individuals were captured, all PCRs were negative but 17% (3/18) had a positive serology. Another study conducted after the epidemic found only one (1/4) three-tooth sloth (*Bradypus tridactylus*) with feces highly infectious for *C. burnetii* MST17. The same strain *C. burnetii* genotype 17 has been laboratory-confirmed in this mammal and in human cases. These results support the implication of three-toed-sloth in this epidemic. Human contamination mainly occurs through inhalation of infectious aerosols as suggested by high relative risk associated with house cleaning activities and pulmonary forms of the disease, and through direct contact with three-toed-sloth. Positive serological results among marsupials confirm wildlife exposure and suggest a more complex sylvatic transmission cycle among wild mammals.

1. Introduction

Q fever, a cosmopolitan zoonosis caused by the intracellular bacterium *Coxiella burnetii*, is a public health concern in Cayenne, the main city of French Guiana, a French overseas entity located on the northeast coast of South America [1,2]. In a prospective study conducted from 1996 to 2000, the mean annual incidence rate was estimated to 37 cases per 100,000 inhabitants, one of the highest in the world [3]. Pneumonia is the primary manifestation of acute Q fever, representing 24.4% of the community-acquired pneumonia admitted to the Cayenne

regional hospital [4]. A unique genotype, *C. burnetii* multispacer sequence type MST17, only isolated from Cayenne to date, is responsible for the disease [5]. Several risk factors have been identified such as living near forested areas and practicing activities resulting in inhalation of aerosols of dusts [3]. In contrast, no link with classical sources of *C. burnetii* (cattle, sheep, or goat birth products) has been ever identified and a wild reservoir has been suspected [2,3,6,7].

The “Camp du Tigre” is a military training camp in the city of Cayenne with a residential area of 18 houses, surrounded by rainforest and located at the top of a hill (Fig. 1). The Camp du Tigre has been

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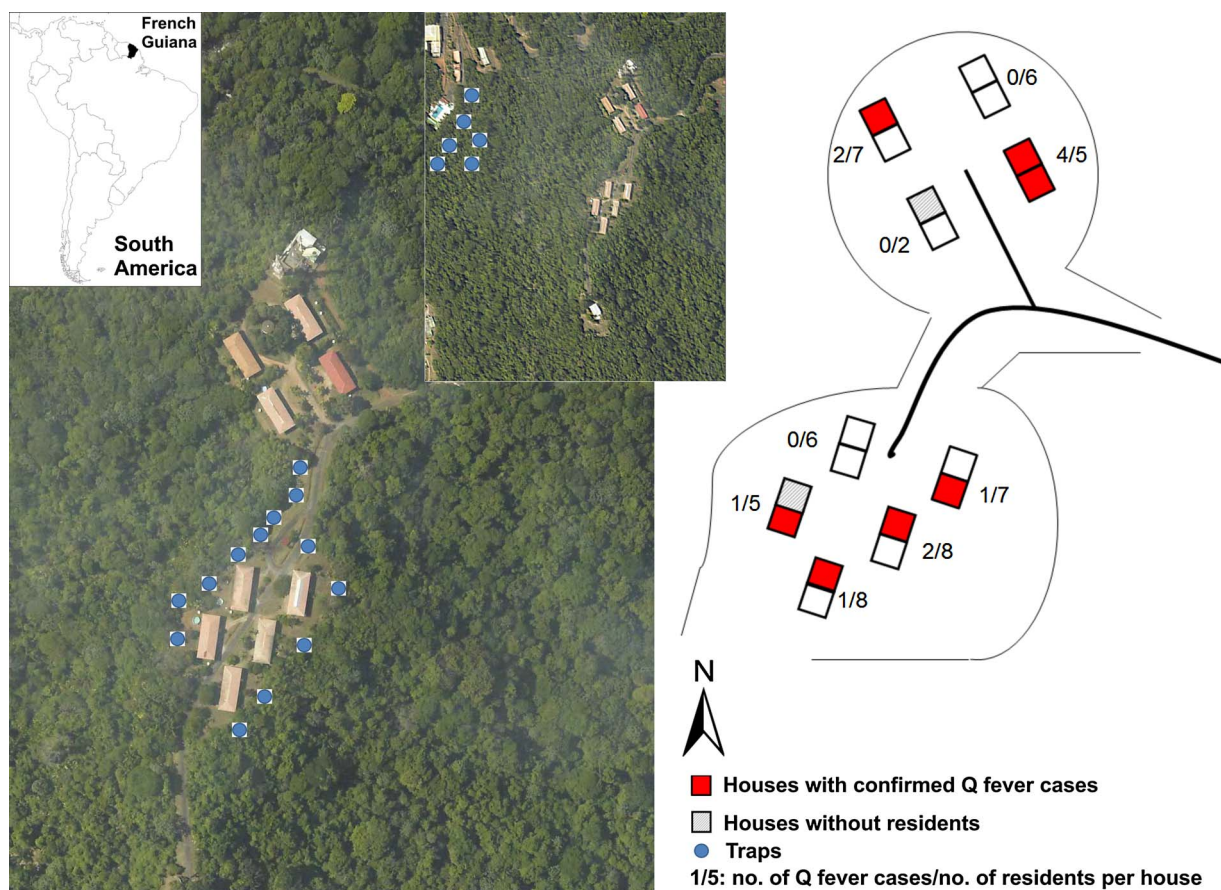


Fig. 1. Camp du Tigre military residential area – Q fever cases distribution in houses. Aerial photography by French armed forces in French Guiana.

specifically identified in a previous study as an area with high Q fever incidence rate, with several cases occurring among military personnel during 1996–2000 [3,8]. In 2004–2005, a Q fever outbreak occurred among military personnel living at the residential area, resulting in a total of 10 Q fever cases (unpublished data). In March 2013, once again one confirmed and two suspected Q fever cases occurred in this population. A study conducted after the outbreak among sheep, goats, wild mammals and birds living on and around the hill found only one (1/4) three-tooth sloth (*Bradypus tridactylus*) with feces highly infectious for *C. burnetii* MST17 and 88% of his ticks were positives for *C. burnetii* using specific PCR [6]. But a link with human cases was not confirmed. We report the results of the investigations conducted during this outbreak.

2. Material and methods

2.1. Epidemiological investigation

Fifty-four inhabitants (20 active military personnel and 34 members of their families) were living in this residential area (Fig. 1). Considering the frequency of asymptomatic Q fever infections and the risk of chronic Q fever, a serological screening based on two samples at least 3 weeks apart, was first systematically proposed to all the inhabitants. In addition, the population was followed up during three months and Q fever diagnosis was systemically performed to any new patient presenting a fever episode ($T^{\circ} \geq 38.5^{\circ}\text{C}$) by indirect immunofluorescence assay serology, one sample taken the first week of illness and a second 3 weeks later. Quantitative real-time polymerase chain reaction (qPCR) targeting the IS1111 sequence on serum and blood samples was also performed as described before [9]. We used lyophilization to concentrate DNA and increase qPCR sensitivity [10]. Then, we genotyped

C. burnetii positive DNA using a specific qPCR for *C. burnetii* MST17 [11]. Any new Q fever case was treated with 200 mg of doxycycline daily during three weeks [4]. Patients were follow-up after treatment, with repeated serology every 6-months. Retrospective cohort study was conducted to identify Q fever risk factors during this outbreak. All the 54 inhabitants were included with their consents in the study and completed a questionnaire containing information on occupation, housing and contacts with animals during the month preceding first serology or the month preceding symptoms for patients with confirmed Q fever. The parents answered for their youngest children. Confirmed acute Q fever case was defined as positive serology (IgM ≥ 50 and phase II IgG ≥ 200) and/or positive qPCR on serum or blood [12]. Elevated phase I IgG titer ($\geq 1:800$) was in favor of persistent focalized Q fever infection and the presence of low phase I and II IgG titer ($\leq 1:400$) without IgM considered as past infection.

2.2. Investigation in wild mammals

As the reservoir of *C. burnetii* is still unknown in French Guiana, we could not speculate on which mammal species (and parturition period) to target. Wild mammals were captured at the study site, up and down the hill, between the 18th and the 23rd of May 2013, using BTTm (BTTm, Besançon Trap Service mécanique, France), Tomahawk (Tomahawk Live Trap Co., Tomahawk, WI) and Sherman traps (Sherman Trap Co., Tallahassee, FL) for a total effort of 138 trap/nights (Fig. 1, Fig. 2). A total of 18 individuals' males and females belonging to two marsupial species were captured: 12 *Didelphis marsupialis* and 6 *Philander opossum*. Whenever possible, blood samples were collected ($n = 18$), vaginal swab ($n = 14$) as well as ticks when present ($n = 15$). *C. burnetii* replicates to very high levels in the placental tissue of infected animals compare to waste products as feces or urine [13].

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