

and Hep-2C derive from the same tissue (human Caucasian larynx carcinoma), while Vero and BGM derive from another organ (Africa green monkey kidney). Thus, Hep-2 and Vero cell lines that we used are likely susceptible to TSV if the virus can infect Hep-2C and BGM as reported by Audelo-del-Valle et al.

The difference between our methods and those used by Audelo-del-Valle et al. may explain the discrepant result. If CPE occurred "usually from 19–23 hours" and "cells were then harvested and lysed" for next injection, TSV most likely persisted in the lysate after the third passage because the cell monolayers had not been washed as they were in our method. According to the time the CPE was observed and the methods of Audelo-del-Valle et al., we assumed that, in their study, cells might be passaged at least three times within 1 week, whereas TSV might remain viable and infective for 1 week. Additionally, the Office International des Epizooties recommended an injection volume of 1% of shrimp body weight (8); Audelo-del-Valle et al. used 10%. With such a large dose, shrimp could be infected easily with TSV from the initial medium and die suddenly. Moreover, the evidence of successful infection from photos of CPE only is not sufficient; Audelo-del-Valle et al. should offer more convincing evidence from images of viral particles in cells by electron microscope or in situ hybridization. Therefore, we think the CPE that Audelo-del-Valle et al. reported was not caused by TSV but by a virus contaminant or some harmful component from shrimp extract.

The structure of the TSV genome is similar to that of small insect-infecting RNA viruses (10), which belong to a renamed virus genus, *Cripavirus* (11). No published reports have shown that other viruses in this genus are able to infect mammalian cells or cell lines. Moreover, TSV is prevalent in shrimp farming

areas in the world, and *L. vannamei* (principal host for TSV) are eaten by people worldwide (8). In China, some persons eat fresh shrimp without disinfecting them; however, no evidence shows that TSV can infect humans. The results of our study show that TSV cannot infect mammalian cell lines or cells.

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Bartonella clarridgeiae and *B. henselae* in Dogs, Gabon

To the Editor: The genus *Bartonella* contains several recently described species, many of which are emerging human pathogens. Human infections are mostly due to *Bartonella henselae* and *B. quintana*. Like many vectorborne disease agents, *Bartonella* species have a natural cycle. This cycle contains a reservoir host, in which *Bartonella* species cause an intraerythrocytic bacteremia, and a vector, which transmits the bacteria from the reservoir host to a new susceptible host (usually the uninfected reservoir host) (1). In the case of *B. quintana* and *B. bacilliformis*, the natural host is human. In *Bartonella* diseases, humans act as accidental hosts. Among the nonhuman *Bartonella* species that infect humans, *B. henselae* is most commonly encountered and usually causes cat-scratch disease. However, several cases of infections in humans attributable to other *Bartonella* species, including *B. elizabethae*, *B. grahamii*, *B. vinsonii arupensis*, *B. vinsonii berkhoffii*, and possibly *B. clarridgeiae*, have been reported (1).

Isolation of *Bartonella* species in animals that have contact with humans can help identify new human pathogens or new diseases. We report results of isolation of *Bartonella* spp. from the blood of 258 dogs in Gabon.

The study was performed in the Ogooué-Ivindo province of Gabon, a country of Central Africa with an equatorial climate. Blood samples were taken from dogs in the town of Mékambo and in all villages connecting Mékambo and Mazingo (nine villages) and Mékambo and Ekata (seven villages) during July and August 2003. Each dog brought by its owner for the study was weighed and sedated by injection with 50 µg/kg of medetomidine (Pfizer Santé Animal, Orsay, France). After the dog was examined, a blood sample was drawn from the jugular vein by Vacutainer (Becton Dickinson, Meylan, France). Each dog was tattooed with an identification number and given both antihelminthic and external antiparasitic treatments. During the examination, the dogs were treated with care; upon completion of the examination, the dogs were given 250 µg/kg of the reversal agent atipamezola (Pfizer Santé Animal) intramuscularly. A physical examination form and a questionnaire were completed for each test participant by its owner. A total of 258 dogs (155 males and 103 females) were examined and had blood samples drawn during the study. All animals were of mixed breeds and were 6 months to 14 years old (average 3 years 1 month). The Vacutainer tubes were kept on ice until blood samples were dispensed into cryotubes and frozen in liquid nitrogen. Samples were stored at -80°C until isolation attempts were made on Columbia agar (Biomérieux, Marcy l'étoile, France) as described previously (2). In this study, six *Bartonella* isolates were obtained and identified as *B. clarridgeiae* (five isolates) and *B. henselae* (one isolate), by

internal transcribed spacer amplification and sequencing (3).

B. vinsonii subsp. *berkhoffii* was the first *Bartonella* species found in dogs (1). Isolation of *B. clarridgeiae* (4,5) and *B. washoensis* (6) in dogs was recently reported. Infection of dogs by other *Bartonella* species was also detected in the DNA of *B. henselae* (7,8), *B. clarridgeiae* (7), and *B. elizabethae* (8). The presence of these *Bartonella* species is not surprising, since *Ctenocephalides felis*, the vector of *B. henselae* in cats, has a wide range of hosts, including the domestic dog. However, attempts to isolate this species in samples collected from 211 dogs in the United Kingdom failed (9). *Bartonella* species are supposedly difficult to isolate in dogs because of a low concentration of bacteria in the blood (1). This supposition was apparent in our study; we identified approximately 100 bacterial colonies per milliliter of blood from three of the six dogs in our study. From the other three dogs in our study, including the dog infected with *B. henselae*, we identified two to four bacterial colonies per milliliter of blood.

Most of the data pertaining to *Bartonella* have been obtained in the United States and Europe. Increasingly, *Bartonella* infections are being reported in Africa, especially in southern Africa (10). We report here the first isolation of *B. henselae* from a dog and the first isolation of *B. clarridgeiae* in Central Africa. That dogs also act as reservoirs of *B. henselae* likely has implications in Africa where HIV infections are prevalent.

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