**Leishmania infantum** Infection in Blood Donors, Northeastern Brazil


Author affiliations: School of Medicine of the Federal University of Ceará, Fortaleza, Brazil (D.C.S. Monteiro, A.Q. Sousa, R.M. Fontes, C.C. Praciano, M.S. Frutuoso, L.C. Matos, M.J. Teixeira, M.M.L. Pompeu); School of Medicine of the University of Fortaleza, Fortaleza (D.M. Lima); Unichristus School of Medicine, Fortaleza (M.S. Frutuoso); University of Virginia School of Medicine, Charlottesville, Virginia, USA (R.D. Pearson)

DOI: http://dx.doi.org/10.32032/eid2204.150065

To the Editor: *Leishmania infantum* is endemic to northeastern Brazil. It is responsible for visceral leishmaniasis (VL), a major emerging health problem in urban areas. Transmission occurs predominantly by the *Lutzomyia longipalpis* sand fly, but transfusion-associated VL, caused by *Lutzomyia longipalpis* (VL), a major emerging health problem in urban areas.

Transmission occurs predominantly by the *Lutzomyia longipalpis* (VL), a major emerging health problem in urban areas.

Transmission occurs predominantly by the *Lutzomyia longipalpis* sand fly, but transfusion-associated VL, caused by *Lutzomyia longipalpis* (VL), a major emerging health problem in urban areas.

The percentages of antibody- or PCR-positive units capable of transmitting *Leishmania* and the outcomes are unknown. Viable *Leishmania* might not be in the blood of all PCR-positive donors, and even when present, the inoculum might be reduced by removal of infected circulating mononuclear phagocytes in the Buffy coat, or parasites might be affected by steps involved in preparation or storage. However, if we consider units that test positive by PCR as being potentially infectious, the number of compulsorily screened infections and were rejected. Of the remaining 351 that were negative for co-infection, 43 (12.2%) were positive for leishmanial IgG and 15 (4.3%) for *Leishmania* spp. DNA. Two donors were positive for both by ELISA and PCR. The prevalence of *Leishmania* infection among blood units accepted for transfusion was 16%.

The results demonstrate a surprisingly high prevalence of *Leishmania* infection in blood donors in Fortaleza, several times higher than that other diseases for which blood is screened (Figure). In a recent study in Salvador, Brazil (9), 5.4% of blood donors had leishmanial antibodies, of which 68% were positive by its PCR targeting kDNA amplification.

Buffy coats from 57 (13.2%) serum samples from 431 donors were positive for leishmanial IgG, and 20 (4.6%) were positive for *Leishmania* spp. DNA. Sequencing of all PCR-positive samples confirmed the *Leishmania* genus. Three donors tested positive by both ELISA and PCR. Overall, the prevalence of leishmanial infection was 17.1% of blood donors. Eighty of the 431 units tested positive for ≥1 of compulsorily screened infections and were rejected. Of the remaining 351 that were negative for co-infection, 43 (12.2%) were positive for leishmanial IgG and 15 (4.3%) for *Leishmania* spp. DNA. Two donors were positive for both by ELISA and PCR. The prevalence of *Leishmania* infection among blood units accepted for transfusion was 16%.

The results demonstrate a surprisingly high prevalence of *Leishmania* infection in blood donors in Fortaleza, several times higher than that other diseases for which blood is screened (Figure). In a recent study in Salvador, Brazil (9), 5.4% of blood donors had leishmanial antibodies, of which 68% were positive by its PCR targeting kDNA amplification.

Buffy coats from 57 (13.2%) serum samples from 431 donors were positive for leishmanial IgG, and 20 (4.6%) were positive for *Leishmania* spp. DNA. Sequencing of all PCR-positive samples confirmed the *Leishmania* genus. Three donors tested positive by both ELISA and PCR. Overall, the prevalence of leishmanial infection was 17.1% of blood donors. Eighty of the 431 units tested positive for ≥1 of compulsorily screened infections and were rejected. Of the remaining 351 that were negative for co-infection, 43 (12.2%) were positive for leishmanial IgG and 15 (4.3%) for *Leishmania* spp. DNA. Two donors were positive for both by ELISA and PCR. The prevalence of *Leishmania* infection among blood units accepted for transfusion was 16%.

The results demonstrate a surprisingly high prevalence of *Leishmania* infection in blood donors in Fortaleza, several times higher than that other diseases for which blood is screened (Figure). In a recent study in Salvador, Brazil (9), 5.4% of blood donors had leishmanial antibodies, of which 68% were positive by its PCR targeting kDNA amplification.

Buffy coats from 57 (13.2%) serum samples from 431 donors were positive for leishmanial IgG, and 20 (4.6%) were positive for *Leishmania* spp. DNA. Sequencing of all PCR-positive samples confirmed the *Leishmania* genus. Three donors tested positive by both ELISA and PCR. Overall, the prevalence of leishmanial infection was 17.1% of blood donors. Eighty of the 431 units tested positive for ≥1 of compulsorily screened infections and were rejected. Of the remaining 351 that were negative for co-infection, 43 (12.2%) were positive for leishmanial IgG and 15 (4.3%) for *Leishmania* spp. DNA. Two donors were positive for both by ELISA and PCR. The prevalence of *Leishmania* infection among blood units accepted for transfusion was 16%.
determine whether recipients of blood from donors who are PCR positive and/or leishmanial antibody positive become infected with *L. infantum*. Persons with advanced AIDS or other immunosuppressive conditions seemingly would be at greatest risk for VL.

In Brazil, legislation requires that all blood for transfusion be tested for *T. cruzi*, hepatitis B and C, *T. pallidum*, human T-cell lymphotropic virus types 1 and 2, and HIV-1 and -2. As additional information becomes available, screening for *L. infantum* also might be advisable to reduce the possibility of the recipient becoming infected, developing VL, and possibly being a reservoir of infection in the community (10), particularly in Ceará and other regions where the prevalence of *L. infantum* infection is high.

**Acknowledgments**

We thank Luciana Carlos for all her help.

This work was supported by CNPq, Brazil (grant 477705/2010-3).

**References**


Address for correspondence: Anastácio Q. Sousa, Rua Nestor Barbosa, 315, Parque Lândia. CEP 60455-610, Fortaleza, Ceará, Brazil; email: aqsousa@gmail.com; Daniela C.S. Monteiro, Rua Suiça, 196, Pires Façanha. CEP 61760-903, Eusébio, Ceará, Brazil; email: daniela.monts@gmail.com

---

**Letter to the Editor:** Four strains of cetacean morbillivirus (CeMV; family *Paramyxoviridae*, genus *Morbillivirus*) have been detected in the global cetacean population: porpoise morbillivirus (1), dolphin morbillivirus (2), pilot whale morbillivirus (PWMV) (3), and Longman’s beaked whale morbillivirus (4). In addition, 2 novel morbilliviruses have been identified in asymptomatic or minimally symptomatic bottlenose dolphins (5). CeMVs can be transmitted to humans, and have resulted in both local and large-scale human morbillivirus outbreaks (6–8). The continued presence of morbilliviruses in the global cetacean population is a cause for concern.

**Author affiliation:** University of Las Palmas de Gran Canaria, Arucas (Las Palmas), Canary Islands, Spain

**DOI:** http://dx.doi.org/10.3201/eid2204.150954

---

**LETTERS**

**Figure.** Comparison of the prevalence of *Leishmania infantum* as tested by PCR and ELISA and of other infections compulsorily tested in 431 blood donors in Fortaleza, state of Ceará, northeastern Brazil. HBV, hepatitis B virus; HCV, hepatitis C virus; HTLV, human T-cell lymphotropic virus; Tc, *Trypanosoma cruzi*; Tp, *Treponema pallidum*.

**Morbillivirus and Pilot Whale Deaths, Canary Islands, Spain, 2015**

Eva Sierra, Antonio Fernández, Cristian Suárez-Santana, Aina Xuriach, Daniele Zucca, Yara Bernaldo de Quirós, Natalia García-Álvarez, Jesús De la Fuente, Simona Sacchini, Marisa Andrada, Josué Díaz-Delgado, Manuel Arbelo

Author affiliation: University of Las Palmas de Gran Canaria, Arucas (Las Palmas), Canary Islands, Spain

DOI: http://dx.doi.org/10.3201/eid2204.150954

---

740 Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 22, No. 4, April 2016