

## EPIDEMIOLOGÍA DE LAS ENFERMEDADES POR RICKETTSIAS

### Epidemiological description of infection with agents of the *Rickettsia* genus in rodents, ectoparasites and humans in the northern coast of Antioquia, Colombia

Juan Carlos Quintero, Andrés Felipe Londoño, Francisco Javier Díaz, Piedad Agudelo, Margarita Arboleda, Juan David Rodas

Universidad de Antioquia, Bello, Colombia  
jkquintero@gmail.com

**Introduction and objectives.** *Rickettsia* is a worldwide rodent-carried tick, flea or lice-borne bacteria, in most cases. In Colombia, few reports have been performed, first in the mid 30s, causing an outbreak in the population of Tobia (Cundinamarca), and from the years 2006 to 2008, on the northern region of Colombia known as Urabá.

Our main goal was to perform an epidemiological description of the infection on the above mentioned endemic area of Colombia.

**Materials and methods.** Samples were obtained from 354 rodents captured from the municipalities of Apartadó, Turbo and Necoclí, and 839 parasites were also collected from 94 of those animals. 220 human sera, and 147 paired samples were also taken from patients with febrile syndromes. An indirect immunofluorescence assay was used to detect rickettsial infection in humans and rodents. Additionally, PCR was performed on liver-DNA from rodents searching for specific genetic sequences of *Rickettsia* genus (*gltA* gene) and spotted fever rickettsias (*OmpA* gene).

**Results.** Captured rodents were classified as *Rattus rattus*, *Rattus norvegicus*, *Mus musculus*, *Zygodontomys cherrei*, *Proechimys semiespinosus* and *Heteromys anomalus*. Likewise, ectoparasites collected from rodents were identified as ticks from the Argasidae and Ixodidae families; fleas from Rophalopsillydae and Pulicidae families; lice from *Gyropus* sp. y *Hoplopleura* sp. genera and mites from *Laelaps* sp. and *Ornithonyssus* sp. genera. We obtained a 6.8% DNA frequency of infection to rickettsias by PCR (*gltA*) for rodents. Only one of these samples of *Amblyomma* sp. was positive by PCR for both genes. 53 human samples were positive for IFA, showing a prevalence of 24% for the spotted fever group

**Conclusions.** The results of this study show circulation of *Rickettsia* genus agents not only on

rodents, but also in vectors and humans from the studied areas. However, species identification still requires additional analysis.

This is the first of a series of studies that will allow us to ecologically characterize this endemic site and possibly recommend the measures to prevent future human cases.



### Pesquisa de infecção por *Rickettsia parkeri* em humanos, equinos, cães, gambás e carrapatos, Município de Paulicéia, Estado de São Paulo, Brasil

Lara Silveira, Fernanda Aparecida Nieri Bastos, Thiago Fernandes Martins, Marlene Olegário, Elizangela Guedes, Marcelo Bahia Labruna

Universidade de São Paulo; Universidade Federal de Uberlândia; Embrapa Gado de Leite, Juiz de Fora. Minas Gerais, Brasil  
iarasilv@yahoo.com.br

**Introducción y objetivos.** A *R. parkeri* causa riquetsiose humana nos E.U.A. No município de Paulicéia, estado de São Paulo, Brasil, havia 9,7% de *A. triste* infectado por *R. parkeri*. Busca de anticorpos anti-*R. parkeri* em humanos, cavalos, cães e gambás e da infecção por *R. parkeri* em carrapatos. Coletas em fevereiro de 2008, março e setembro de 2009.

**Materiales y métodos.** Para a técnica de reação de imunofluorescência indireta o ponto de corte era  $\geq 64$ , com os antígenos: *R. rickettsii*, *R. parkeri*, *R. bellii*, *R. amblyommii*, *R. rhiphcephalii* e *R. felis*. Os carrapatos foram testados pela PCR para o gene *gltA* de *Rickettsia*.

**Resultados.** Apresentaram anticorpos anti-*R. rickettsii* e *R. parkeri*: 1 (4%) de 26 soros de humanos, títulos  $\geq 64$ ; 34 (24%) de 140 soros de equinos, títulos 64 a 1024; 5 (7,7%) de 55 amostras de cães, títulos 64 a 256. Para 9 equinos e 2 cães a *R. parkeri* foi o provável antígeno homólogo (diferença entre títulos de 4 vezes). De 1593 carrapatos 43 (2,7%) eram adultos e destes 41 (95%) *A. cajennense* e 2 (5%) *A. coelebs*. De 985 ninfas (62% do total), 980 (99,5%) *A. cajennense*, 4 (0,4%) *A. coelebs* e 1 (0,1%) *A. triste*. 565 (35% do total) eram larvas: 480 (85,0%) *A. cajennense*, 55 (9,7%) *R. B. Microplus*, 20 (3,5%) *A. dubitatum*, e 10 (1,8%) *D. nitens*. Somente 2 ninfas de *A. coelebs* continham DNA riquetsial, 100% de identidade