Potential vectors and hosts of <em>Rickettsia</em> spp: epidemiological studies in the Vale do Paraíba, state of Rio de Janeiro/Brazil

G. S. Gazeta<sup>1</sup>, E. R. Souza<sup>2</sup>, A. E. Abboud-Dutra<sup>1</sup>, M. Amorim<sup>1</sup>, P. R. Barbosa<sup>3</sup>, A. B. Almeida<sup>3</sup>, V. Gomes<sup>3</sup>, F. S. Gehrze<sup>2</sup>, M. T. Marrelli<sup>2</sup> and T. T. S. Schumaker<sup>2</sup>

<sup>1</sup>Instituto Oswaldo Cruz, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil, <sup>2</sup>Departmento de Parasitolologia, Universidade de são Paulo, São Paulo, Brazil and <sup>3</sup>Coordenação de Vigilância em Saúde, Secretaria de estado de Saúde e Defesa Civil do Rio de Janeiro, RJ, Brazil

INTRODUCTION

Brazilian spotted fever (BSF) is a rickettsiosis very similar to the Rocky Mountain spotted fever also caused by <em>Rickettsia rickettsii</em>, which is sustained in nature in a cycle involving vectors and mammals [1]. The state of Rio de Janeiro, with one of the highest population densities in Brazil, has one of the highest numbers of BSF cases. However, information about the epidemiology of this disease is lacking. The objectives of the present work were to analyse <em>Rickettsia</em> spp. in the host and vectors collected in municipalities of the Vale do Paraíba, where BSF fatal cases were recently recorded.

METHODS

Sera were collected from domestic animals resident in areas of Resende, Barra Mansa, Barra do Piraí and Valença (municipalities of Vale do Paraíba, Rio de Janeiro) with occurrence of BSF cases. Ticks and fleas were removed from different hosts and humans. The sera were tested by indirect immunofluorescence assay (IFA), using <em>Rickettsia rickettsii</em> as antigen. The vector samples were compounded by one to five specimens, which were pooled according to species, sex and the host they were removed from.

Genomic DNA was extracted and polymerase chain reaction (PCR) was performed using primers to the rickettsial genes <em>glt</em>A (381pb) and <em>omp</em>A (532pb) [2].

According to Margolis <em>et al</em. and Serra-Freire [3,4], the following ecological rate values were determined: similarity (SR) (degree of similarity among potential vectors of two municipalities); dominance (DR) (percentage of one species related to all potential vectors of one municipality); abundance (AR) (availability of the potential vectors in determined municipality); equitability (ER) (regularity of the diversity of one municipality); parasitic association (PA) (used to recognise the occurrence of interspecific association that manifests independently of its variation and abundance); and prevalence (relation among the number of individuals, or pools of individuals, considered reacting to one determined test, i.e. PCR, IFA, and the total analysed number).

RESULTS

In total, 109 sera were collected from dogs (61), equines (34), bovines (13) and cats (01). The sera-positive animals were: dogs (58.7%), equines (44.1%), bovines (15.4%) and cats (100%). PCR positive to rickettsial gene fragments were: dogs (13.1%) from Barra do Piraí and Valença, and equines (8.8%) from Barra do Piraí.

Regarding vectors, the 704 collected samples were identified as the following species: 174 <em>Amblyomma cajennense</em> (24.7%), 225 <em>Rhipicephalus sanguineus</em> sanguineus (31.9%), 147 <em>Clenocephalides felis</em> (20.9%), 26 <em>Amblyomma</em> sp. (3.7%), 3 <em>Amblyomma aureolatum</em> (0.4%), 36 <em>Anocentor nitens</em> (5.1%), and 93 <em>Boophilus microplus</em> (13.2%).

We analysed the DNA extracted from 218 vector pools (n = 321), and 14.2% of them yielded rickettsial gene fragments by PCR. The prevalence of PCR reactive pools was: <em>R. sanguineus</em> (30.0%), <em>A. cajennense</em> (5.3%), <em>A. aureolatum</em> (33.3%) and <em>C. felis</em> (16.4%). PCR technique showed infected vectors in Barra Mansa (<em>C. felis</em>, <em>R. sanguineus</em>, <em>A. cajennense</em>), Barra do Piraí (<em>C. felis</em>) and Resende (<em>C. felis</em>, <em>R. sanguineus</em>, <em>A. cajennense</em>, <em>A. aureolatum</em>). The SR values among the vector’s fauna of the studied municipalities ranged from 0.6 to 0.8. Taking into account only <em>A. cajennense</em>, <em>R. sanguineus</em> and <em>C. felis</em> species (the most frequent and PCR-reactive species), the SR values ranged from 0.8 to 1.0. The values of DR were 31.9, 24.7 and 20.8, respectively, for <em>R. sanguineus</em>, <em>A. cajennense</em>
DISCUSSION

Although the number of BSF cases has been increasing in the state of Rio de Janeiro, almost nothing is known about the vectors and hosts of BSF.

Using PCR, *Rickettsia* spp. were detected infecting vectors in all municipalities excepting Valença. However, in this municipality, rickettsial gene fragments were detected in dogs by using the same molecular technique. Rickettsial genes were also detected in equine sera from Barra do Piraí. These findings suggest that domestic animals can act as important sources of rickettsial agents to the vectors.

In the studied areas dogs were strongly associated with *R. sanguineus*, *A. cajennense*, and *C. felis*, whereas equines were associated with *A. cajennense*. The *A. cajennense* tick species is considered the most important vector of BSF to humans. Indeed, we detected spotted fever group rickettsiae (*ompA* gene amplification) in a sample collected from humans.

The epidemiological data suggest that in the eastern and western parts of the Vale do Paraíba, the most important vectors are *R. sanguineus* and *A. cajennense*, respectively. Dogs, horses and their ectoparasites seem to be crucial in the maintenance of the peridomiciliary enzootic cycle of *Rickettsia* spp., and potentially are responsible for the human epizootic events observed in the region. To better clarify the epidemiology of *Rickettsia* spp. in the region, the analysis of nucleotide sequences of all PCR amplified products is in progress. The data obtained in the present work have been used to improve the strategies for tick/rickettsiosis control in the region by the Public Health Services.

CONCLUSION

This is the first epidemiological BSF study developed in the State of Rio de Janeiro/Brazil, using serological and molecular methodologies. Our results indicate the participation of dogs, equines, *R. sanguineus*, *A. cajennense* and *C. felis* in the maintenance of the peridomiciliary enzootic cycle of *Rickettsia* spp. These vectors and hosts are potentially responsible for the human epizootic events in the studied municipalities.

ACKNOWLEDGEMENTS

Supported by FAPESP/CNPq/CAPES.

REFERENCES