cropland areas are associated with high risk for infection(*2*,*3*,*6*). Northeast Jeju Island, which includes SH, AW, and HD, has many farms and wetlands, and the IR of SFTSV in ticks peaked there in July, August, and September. In addition, SFTSV was detected in ticks in winter on Jeju Island, but no SFTS cases were reported in South Korea during winter. The 62 confirmed SFTS cases were statistically significantly associated with higher ambient temperature (22.5°C ±4.2°C) compared with patients with negative RT-PCR results for SFTSV (18.9°C ±5.7°C; p<0.001) (J.R. Yoo, unpub. data). The optimal temperature range for growth and reproduction of *H. longicornis* ticks is 20°–24°. Jeju Island maintains a temperature >20° during May–October and is largely a rural and natural environment. We consider this area to have the highest prevalence of SFTS cases and ticks with SFTSV in South Korea.

The results of this study showed that Jeju Island has the highest IR of SFTSV in ticks compared with other regions of South Korea and endemic countries. In addition, we found that the partial small segment of SFTSV in ticks was highly homologous to SFTSV in patients on Jeju Island and that Northeast Jeju Island, which includes SH, is a high-risk area for human SFTS infections.

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About the Author

Dr. Yoo and Dr. Heo are professors in the Department of Internal Medicine, Jeju National University, College of Medicine, Jeju, South Korea. Their research interests are infectious diseases.

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Address for correspondence: Keun Hwa Lee, Department of Microbiology, Hanyang University College of Medicine, 222 Wangsimni-ro Seongdong-gu, Seoul 04763, South Korea; email: yomust7@gmail.com

Typhus Group Rickettsiosis, Brazilian Amazon

Antonio H.H. Minervino, Marcelo B. Labruna, Salatiel R. Dias, Francisco B. Costa, Thiago F. Martins, Phablo N.S. da Silva, Álvaro A. Faccini-Martínez

Author affiliations: Federal University of Western Pará, Santarém, Brazil (A.H.H. Minervino, S.R. Dias, P.N.S. da Silva); University of São Paulo, São Paulo, Brazil (M.B. Labruna, T.F. Martins); Universidade Estadual do Maranhão, São Luís, Brazil (F.B. Costa); Asociación Colombiana de Infectología, Bogotá, Colombia (Á.A. Faccini-Martínez)

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Rickettsia rickettsii infection is the only rickettsiosis included in the list of reportable diseases in Brazil, where typhus group rickettsioses, mainly murine typhus, have been underreported. We report a case of typhus group rickettsiosis with unique ecologic particularities in a patient from the Brazilian Amazon, where, to our knowledge, rickettsioses have not been reported.

Typhus group rickettsioses are vectorborne infectious diseases that include murine typhus, caused by *Rickettsia typhi*, and epidemic typhus, caused by *R. prowazekii* (*1*). *R. typhi* is maintained in an enzootic cycle involving small mammals (e.g., *Rattus* spp. rats and *Didelphis* spp. opossums) and their ectoparasites, mainly fleas (*2*). *R. typhi* is usually transmitted to humans by contamination of the bite site, mucosal or skin abrasions with rickettsia-containing ectoparasite feces, or inhalation in contaminated dust (*2*). *R. prowazekii* is transmitted mainly by feces of human clothing lice (*Pediculus humanus humanus*) or a sylvatic cycle in the United States by contact with ectoparasites of flying squirrels (*1*).

In Brazil, there have been few reports of murine typhus, mostly >60 years ago and all from human-modified landscapes in southeastern or southern regions, far from the Amazon (*3*). To our knowledge, Brazil has had only 1 case of recrudescent, epidemic typhus (Brill-Zinsser disease) in a refugee from Europe (*4*). Currently, Brazilian spotted fever (*R. rickettsii* infection), a tickborne disease, is the only rickettsiosis included in the list of notifiable diseases in Brazil (*3*). We report a new case of typhus group rickettsiosis in a patient from the Brazilian Amazon.

On August 27, 2019, a 37-year-old man was admitted to a hospital at Porto Trombetas District (Pará State, eastern Amazon region of Brazil) (Figure) because of 4 days of fever, chills, headache, malaise, and productive cough, associated with mild respiratory distress 72 hours after fever onset. His daily work consisted of outdoor herpetologic monitoring activities in Saracá-Taquera National Forest (35 km from Porto Trombetas) during the 2 weeks before disease onset. He reported that while in the forest, he removed an attached tick from his right thigh 10 days before disease onset.

Physical examination showed fever (temperature 38.3°C), tachycardia, tachypnea, O_2 saturation 91%, bilateral inguinal lymphadenopathy, no rash, and a furuncle lesion at the site of the tick bite on the right thigh, and no inoculation eschar. Blood analysis showed leukocytosis (15,000 cells/mm^3); neutrophilia (84%); standard platelet count (221,000 platelets/μL); and increased levels of alanine aminotransferase (50 U/L), aspartate aminotransferase (38 U/L), and C-reactive protein (20 mg/L). Chest radiograph showed bilateral interstitial pulmonary infiltrates. Presumptive diagnoses of Lyme borreliosis or Brazilian spotted fever was made and the patient was admitted.

Supplementary oxygen, ceftriaxone, chloramphenicol, and doxycycline were administered, and serologic tests for *Borrelia burgdorferi* and *Rickettsia* spp. were performed. Twenty-four hours later, the patient showed clinical stability, major improvement of respiratory status, and no fever. After 7 days of antimicrobial drug treatment, he was discharged with complete resolution of symptoms.

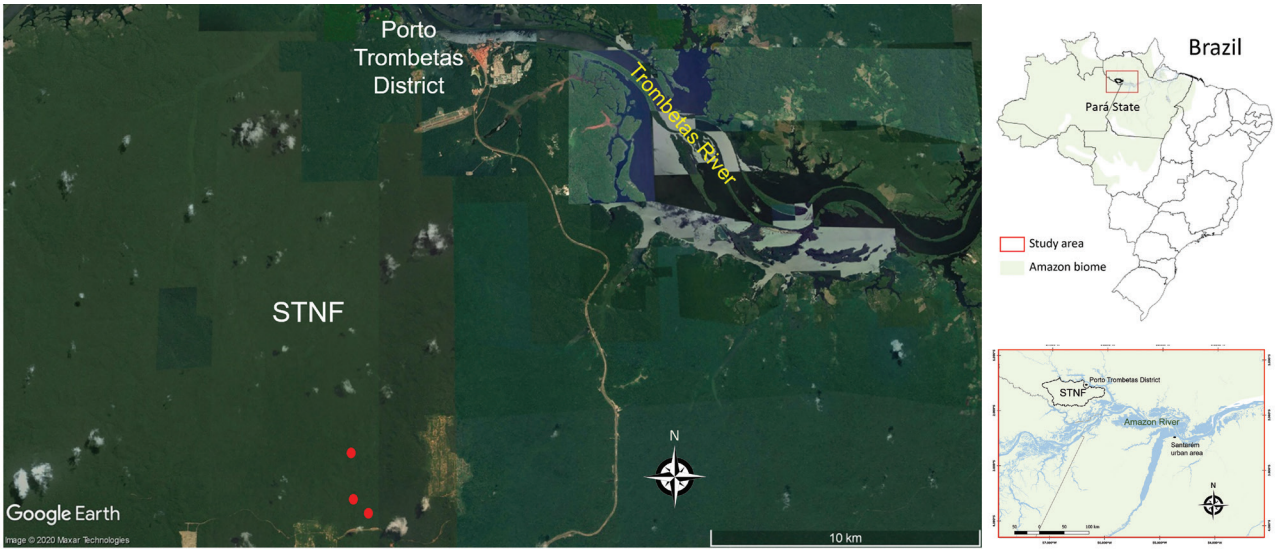

Figure. Study site in which typhus group rickettsiosis was detected in a 37-year-old man, Brazilian Amazon. Red dots indicate sites in STNF in which the patient worked during the day in the 2 weeks before disease onset. During this same period, he spent the night at his house in Porto Trombetas District, where he denied any rat infestation. Insets show location of STNF in Pará state and Brazil. STNF, Saracá-Taquera National Forest.

A serum sample collected on August 28 (5 days after disease onset) showed negative results by commercial ELISA for *B. burgdorferi* IgM and IgG. Results of indirect fluorescent antibody assays were nonreactive for *R. conorii* IgG but positive (titer 1:64) for *R. typhi* IgG.

To confirm a presumptive diagnosis of rickettsiosis, we collected a second serum sample 2 months later and showed by using an in-house indirect fluorescent antibody assays (*5*) negative results for IgG (titer <1:64) against 6 *Rickettsia* species: *R. felis*; *R. bellii*; and the spotted fever group agents *R. rickettsii*, *R. parkeri*, *R. amblyommatis*, and *R. rhipicephali*. This serum sample had a titer of 1:2,048 against *R. typhi* (Wilmington strain), confirming typhus group rickettsiosis.

There have been previous reports of typhus group rickettsiae in ticks from other areas (*6*,*7*). After we considered the tick bite history of the patient, during October 12–14, 2019, we went to areas in Saracá-Taquera National Forest that the patient visited and collected 170 ticks in 7 species. Attempts to detect rickettsial DNA in these ticks showed only *R. amblyommatis* in *Amblyomma cajennense* sensu stricto ticks (Appendix, https://wwwnc.cdc.gov/EID/article/26/9/20-1305-App1.pdf).

In a retrospective interview, the patient recalled 3 additional activities during the 2 weeks before disease onset: a daily rest in the forest for a few minutes after work, seeking work materials in a small mammal trap-storage at a facility within the natural forest, and 2 short visits to his mother's house in the urban area of Santarém municipality (Pará State). He denied rat infestation in his own house at Porto Trombetas but reported previous rat infestations in his mother's house.

Borreliosis and rickettsioses have not been confirmed in the Brazilian Amazon (*8*). The patient's tick bite history before onset of symptoms led clinicians to presume these diagnoses and initiate appropriate antimicrobial drug treatment (e.g., doxycycline) (*1*), with a successful outcome. Because *R. amblyommatis*, a possibly nonpathogenic species (*1*), was the only agent detected in collected ticks, we consider that the furuncle lesion at the site of the tick bite was a pyogenic, localized, skin infection, and not rickettsia related.

Because of similar clinical manifestations and serologic cross-reactions between typhus group rickettsiae (*1*), we could not confirm the typhus group etiologic agent of this case-patient. We presume *R. typhi* as a probable infection because he had potential occupational exposures with rodents or other small mammals and their ectoparasites, rather than clothing louse infestation (*1*), in addition to an absence of neurologic symptoms, which are more common for epidemic typhus than for murine typhus (*9*,*10*). Conversely, the fact that the patient had spent most of his time in a forest environment could also implicate a sylvatic cycle of typhus group rickettsia in the Amazon forest.

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About the Author

Dr. Minervino is an associate professor at the Federal University of Western Pará, Santarém, Brazil. His research interests include epidemiology of tick-borne diseases.

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Address for correspondence: Álvaro A. Faccini-Martínez, Asociación Colombiana de Infectología, Carrera 15 No.118-03, Bogotá, Colombia; email: afaccini@gmail.com

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Typhus Group Rickettsiosis, Brazilian Amazon

Appendix

Collection and Identification of Ticks in Amazon Forest Area Visited by the Febrile Patient

On October 2019, we collected host-questing ticks by flagging the vegetation in the patient-visited areas in the Saracá-Taquera National Forest, Porto Trombetas District, Brazilian Amazon. In addition, we collected ticks from a fresh carcass of an agouti (*Dasyprocta leporina*) that was found in the area. Collected ticks were transported alive to the laboratory, where they were identified to species according to the procedure of Dantas-Torres et al. (*1*). A total of 170 ticks were identified in 7 species, including 6 *Amblyomma* spp. (Appendix Table).

For molecular detection of rickettsiae, we processed ticks individually (adults and few nymphs) or in pools of 2 to 10 ticks (most of the nymphs) by using the guanidine isothiocyanate phenol technique (*2*) and tested by using PCR and primers CS-78 and CS-323 targeting a 401-bp fragment of the citrate synthase gene, which is common in all representatives of the genus *Rickettsia* (*3*). Samples yielding expected size amplicons were subsequently tested with primers Rr190.70p and Rr190.701n, targeting a 631-bp fragment of the rickettsial 190-kDa outer membrane protein gene, which is present only in members of the spotted fever group (*4*). A negative control tube containing ultrapure water and a positive control tube containing DNA of *Rickettsia vini* were included in each PCR run (*5*). Obtained amplicons were treated with ExoSap (US Biochemicals, https://www.thermofisher.com) and DNA-sequenced in an ABI automated sequencer and model ABI 3500 Genetic Analyzer (Applied Biosystems/Thermo Fisher Scientific, https://www.thermofisher.com) with the same primers used for PCR. Acquired sequences were assembled with Geneious R9 software (https://www.geneious.com) and subjected to blast analyses (https://www.ncbi.nlm.nih.gov) to infer the closest similarities available in GenBank.

The 170 ticks were tested in 50 samples (16 individual adults, 4 individual nymphs and 30 nymphal pools), from which only 17 samples of *A. cajennense* sensu stricto yielded amplicons by both the citrate synthase gene and 190-kDa outer membrane protein gene PCRs. PCR products from these 17 samples yielded DNA sequences that showed 100% identity with *R. amblyommatis* (GenBank accession no. CP012420).

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Appendix Table. Ticks collected in study of typhus group rickettsiosis, Brazilian Amazon*

Tick species	Source	No. specimens collected	No. samples tested	No. samples yielding rickettsial DNA (% infection)
Amblyomma cajennense sensu stricto	Vegetation	9 adults	9	5 (55)
	Vegetation	100 nymphs	11 pools	11 (11)†
	Agouti	10 nymphs	1 pool	1 (10)†
Amblyomma coelebs	Vegetation	9 nymphs	7 pools	0
Amblyomma naponense	Vegetation	1 adult	1	0
	Vegetation	7 nymphs	3 pools	0
Amblyomma oblongoguttatum	Vegetation	3 adults, 2 nymphs	5	0
Amblyomma pacae	Agouti	2 nymphs	1 pool	0
Amblyomma scalpturatum	Vegetation	3 adults	3	0
	Vegetation	22 nymphs	7 pools	0
Haemaphysalis juxtakochi	Vegetation	2 nymphs	2	0
Total	NA	170	50	17

*NA, not applicable.
†% infection, in this instance, refers to minimal infection rate (≥1 infected tick in each pool): no. infected pools/total no. tested ticks x 100.