Rickettsia rickettsii in Amblyomma patinoi Ticks, Colombia

Álvaro A. Faccini-Martínez, Francisco B. Costa, Tatiana E. Hayama-Ueno, Alejandro Ramírez-Hernández, Jesús A. Cortés-Vecino, Marcelo B. Labruna, Marylin Hidalgo

Author affiliations: Pontificia Universidad Javeriana, Bogotá, Colombia (A.A. Faccini-Martínez, M. Hidalgo); Universidade de São Paulo, São Paulo, Brazil (F.B. Costa, T.E. Hayama-Ueno, M.B. Labruna); Universidad Nacional de Colombia, Bogotá (A. Ramírez-Hernández, J.A. Cortés-Vecino)

Address for correspondence: R. Gordon Huth, University of Texas Southwestern Residency Programs, 601 E 15th St, Austin, TX 78701, USA; email: ghuth@seton.org

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To the Editor: Rickettsia rickettsii is the etiologic agent of Rocky Mountain spotted fever (RMSF), a highly lethal tick-borne rickettsioses restricted to the Western Hemisphere (1,2). In Colombia, R. rickettsii was first reported during the 1930s, when 62 (95%) of 65 affected persons died of RMSF in Tobia town (Cundinamarca Department) (3), from where highly virulent strains of R. rickettsii were isolated through the inoculation of patient blood or of Amblyomma cajennense sensu lato (s.l.) extracts into guinea pigs (4). Thereafter, RMSF remained unnoticed in Colombia until the 21st century, when new outbreaks with high case-fatality rates were reported in different regions, including Villeta, a nearby locality of Tobia (1).

Recent studies have shown that A. cajennense s.l., widely distributed from the southern United States to Argentina, is actually a complex of 6 different species: A. cajennense sensu stricto (Amazonian region), A. mixtum (from Texas, USA, to western Ecuador), A. sculptum (northern Argentina, Bolivia, Paraguay, Brazil), A. interandinum (inter-Andean valley of Peru), A. tonelliae (dry areas of northern Argentina, Bolivia, and Paraguay), and A. patinoi (eastern cordillera of Colombia) (5). With this new classification, A. patinoi, originally described from Villeta, is the only species of this complex known to occur in the RMSF-endemic area of Cundinamarca, Colombia (5).

In August 2013, we collected 15 A. patinoi adult ticks from cattle in Naranjal village (5°3′31.52″N, 74°26′50.24″W), Villeta town, an area of Cundinamarca, Colombia, to which RMSF is endemic. Ticks were taken alive to the laboratory, where they were frozen at –80°C for further analysis. The 15 ticks were defrosted, surface sterilized with iodine alcohol, and processed individually by the shell vial technique for isolation of rickettsiae in Vero cells, as described (6). Infected cells were always incubated at 28°C. Rickettsiae were observed by Gimenez staining within cells (online Technical Appendix Figure 1, http://wwwnc.cdc.gov/EID/article/21/3/14-0721-Techapp1.pdf) from only 1 (inoculated from a female tick) of the 15 inoculated shell vials. This isolate was subjected to at least 7 Vero cell passages, each achieving >90% infected cells.

DNA was extracted from an aliquot of first passage–infected cells and tested by a battery of PCR protocols targeting fragments of the rickettsial genes gltA, ompA, and ompB and the intergenic regions RR0155-rpmb, RR1240-tlc5, and cspa-ksgA (Table). We sequenced 1,106 bp, 512 bp, and 799 bp of the gltA, ompA, and ompB genes, respectively. By BLAST analyses (http://www.ncbi.nlm.nih.gov/blast), these sequences were 100% identical to corresponding sequences of R. rickettsii from Colombia and Brazil (GenBank accession nos. CP003306, CP003305). Generated sequences for 2 intergenic regions, RR0155-rpmb (228 bp) and RR1240-tlc5 (306 bp), were 100% identical to corresponding sequences of the same 2 R. rickettsii isolates from Colombia and Brazil. A 337-bp sequence of the cspa-ksgA intergenic region was 100% (337/337 nt) identical to R. rickettsii from Brazil (CP003305) and 99.7% (336/337) to R. rickettsii from Colombia (CP003306). Partial sequences from R. rickettsii generated in this study were deposited into GenBank and assigned nucleotide accession nos. KJ735644–KJ735649.

Whole-body remnants of the 15 ticks used to inoculate shell vials were also subjected to DNA extraction and processed by PCR for the rickettsial gltA gene (Table); only 1 tick (the one that provided the rickettsial isolate) contained rickettsial DNA, indicating a 6.6% (1/15) infection rate. We confirmed the taxonomic identification of this
tick as *A. patinoi* by generating mitochondrial 16S rRNA partial sequences from it and from an *A. patinoi* paratype that is deposited in the tick collection of the University of São Paulo (Brazil) (accession no. CNC-1585) (5). Both sequences were 100% identical to each other (deposited in GenBank under accession nos. KP036466–KP036467).

A 3 mL-aliquot of the second infected cell passage was inoculated intraperitoneally into an adult male guinea pig, in which high fever (rectal temperature >40.0°C) developed during days 5–8 days post inoculation. A total of 3 guinea pig passages were performed, always followed by high fever. A second passage animal survived; scrotal necrosis developed (online Technical Appendix Figure 2), and this animal seroconverted to *R. rickettsii* with 32,768 endpoint IgG titer (online Technical Appendix Figure 2), and this animal sequence was 100% identical to each other (deposited into 5 São Paulo (Brazil) (accession no. CNC-1585) (5). Both sequences were 100% identical to each other (deposited in GenBank under accession nos. KP036466–KP036467).

A highly pathogenic strain of *R. rickettsii* was isolated from an *A. patinoi* specimen collected at Villeta, where recent human cases of RMSF have been reported (1). More than 70 years ago, the only previous *R. rickettsii* tick isolates in Colombia were obtained from *A. cajennense* s.l. in Tobia, only 20 km from Villeta (4). At that time, ticks of the *A. cajennense* complex were considered natural vectors of *R. rickettsii* in Tobia (4). Because the *A. cajennense* s.l. complex was recently found to be represented in the eastern cordillera of Colombia (which includes Tobia and Villeta) by the species *A. patinoi* (5), the tick isolates obtained >70 years ago also are highly likely to have been obtained from *A. patinoi*. Therefore, *A. patinoi* ticks should be considered the main vector of *R. rickettsii* to humans in this region of Colombia.

### References
7. Eremeeva M, Yu X, Raoult D. Differentiation among spotted fever group rickettsiae species by analysis of restriction fragment

### Table. Primer pairs used for amplification of rickettsial genes or intergenic regions, Colombia, August 2013

<table>
<thead>
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<th>Target, primer pairs, primers</th>
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The emerged mycobacterial laboratory for BCG detection (<5 years of age have been sent to the national refer-
losis strains and pathologic specimens collected from chil-
since 2008, the isolated extrapulmonary tubercu-
yko-172 vaccine strain spoligotyping, was established in
a laboratory program to differentiate BCG from other spe-
for compensation during 2009–2012 (Figure). In Taiwan,
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applying 8 who were previously reported (1), were identified
to chest radiographs, except for 1 child with rib

To the Editor: Thirty-eight patients with Mycobacte-
BGC-associated osteomyelitis/osteitis, including
8 who were previously reported (1), were identified
during Taiwan’s vaccine injury compensation program
during 1989–2012; a total of 30 (79%) patients applied
for compensation during 2009–2012 (Figure). In Taiwan,
a laboratory program to differentiate BCG from other spe-
cies of the M. tuberculosis complex, using a kit for the To-
kyo-172 vaccine strain spoligotyping, was established in
2004 (1). Since 2008, the isolated extrapulmonary tubercu-
losis strains and pathologic specimens collected from chil-
ren <5 years of age have been sent to the national refer-
ence mycobacterial laboratory for BCG detection (2). The
detected incidence of BCG osteitis/osteomyelitis increased
from 3.68 cases per million vaccinations during 2002–2006
to 30.1 per million during 2008–2012.

Parents or guardians signed written consent forms on
behalf of the children when they submitted claims for the
vaccine injury compensation program. After consent, chil-
ren’s hospital information was stored in the Taiwan Cen-
ters for Disease Control database and used for research.

Of the 38 compensated BCG osteomyelitis/osteitis pa-
tients, 18 were boys. According to chart review, no patients
had immunodeficiency or other underlying conditions;
however, 3 were premature babies (born at 34–36 weeks
of gestation). Eighteen (47%) children had received BCG
at ≤1 week of age, 12 (32%) at 1–4 weeks, 7 (18%) at 1–2
months, and 1 at ≥2 months. The average age at inocula-
tion was 16.2 ± 16.6 days. Symptoms or signs began 3–32
months (average 12.4 ± 6.1 months) after BCG vaccina-
tion; for 68%, symptoms or signs developed 7–18 months
after vaccination (online Technical Appendix Figure, http://
Time from vaccination to onset of symptoms or signs did
not differ for the 3 premature infants.

As in previous reports (3,4), extremity bones were
more commonly involved than axial bones. For 30 (79%)
children, extremity bones were involved: 14 right lower
limbs, 7 left lower limbs, 6 left upper limbs, and 3 right up-
per limbs. The tibia was the most common site (9 patients),
followed by ankle bones (8 patients), femur (4 patients),
radius and thumb (3 patients each), humerus and knee (2
patients each), and ulna (1 patient). Of these, 2 patients had
2 bony lesions. In 8 (21%) children, axial bones were in-
volved: 5 sternums, 2 thoracic vertebrae, and 1 right rib.
Presentation included a mass (25 [66%] children), tenderness
(22 [58%]), limping (19 [50%]), redness (14 [37%]), and
heat (7 [18%]). Average time from first clinical visit to
final surgical management was 1.6 ± 2.1 months.

Eight (53%) of 15 patients had positive tuberculin
skin test results. No specific abnormalities were found
with regard to blood cell counts and inflammation mark-
ers or to chest radiographs, except for 1 child with rib

Mycobacterium bovis
BCG–Associated
Osteomyelitis/Osteitis,
Taiwan

Nan-Chang Chiu, Meng-Chin Lin, Wen-Li Lin,
Shin-Yi Wang, Hsin Chi, Li-Min Huang,
Ren-Bin Tang, Yhu-Chering Huang,
Ching-Chuan Liu, Fu-Yuan Huang, Tzou-Yien Lin

Author affiliations: Mackay Memorial Hospital, Taipei, Taiwan
(N.-C. Chiu, M.-C. Lin, W.-L. Lin, H. Chi, F.-Y. Huang); Mackay
Junior College of Medicine, Nursing and Management, Taipei
(N.-C. Chiu, H. Chi); Taiwan Centers for Disease Control, Taipei
(S.-Y. Wang); National Taiwan University Hospital, Taipei
(L.-M. Huang); Cheng Hsin General Hospital, Taipei (R.-B. Tang);
Chang Gung Memorial Hospital, Taoyuan, Taiwan (Y.-C. Huang,
T.-Y. Lin); National Cheng Kung University Hospital, Tainan,
Taiwan (C.-C. Liu); Ministry of Health and Welfare, Executive
Yuan, Taipei (T.-Y. Lin)

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Figure. Number of patient applications for compensation as
a result of Mycobacterium bovis BCG osteomyelitis/osteitis to
vaccine injury compensation program, Taiwan, 1998–2012.
Rickettsia rickettsii in Amblyomma patinoi
Ticks, Colombia

Technical Appendix

Technical Appendix Figure 1. Rickettsia rickettsii isolated from an Amblyomma patinoi tick, Villeta, Colombia, August 2013. Second passage of infected Vero cells that were inoculated with infected tick extract through the shell vial technique. Gimenez staining, original magnification ×100.
Technical Appendix Figure 2. Scrotal necrosis in a guinea pig that had been inoculated with *Rickettsia rickettsii*–infected Vero cells 14 days previously.