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. interandium* (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 Villa, 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), Villa 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*5, 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*5 (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

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**Rickettsia rickettsii in Amblyomma patinoi Ticks, Colombia**

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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 city (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 Villa, a nearby locality of Tobia (1).
Therefore, A. patinoi also are highly likely to have been obtained from cies of Colombia (which includes Tobia and Villeta) by the spe-
was recently found to be represented in the eastern cordillera 4
jennense R. rick-
complex were considered natural vectors of to humans in this region of Colombia.

4 only 20 km from Villeta (A. cajennense in Colombia were obtained from s.l. in Tobia,
than 70 years ago, the only previous tick isolates R. rickettsii vector of to humans in this region of Colombia.

4 More 
that is deposited in the tick collection of the University of São Paulo (Brazil) (accession no. CNC-1585) (5). Both se-
sequences were 100% identical to each other (deposited into 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 in which high fever (rectal temperature >40.0°C) developed during days 5–8 days post inoculation. A total of 3 guinea pig
inoculated intraperitoneally into an adult male guinea pig,

A highly pathogenic strain of R. rickettsii was isolated from an A. patinoi specimen collected at Villeta, where re-
cent 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. cajen
nese s.l. in Tobia, only 20 km from Villeta (4). At that time, ticks of the A. cajen
nese complex were considered natural vectors of R. rickettsii in Tobia (4). Because the A. cajen
nese s.l. complex was recently found to be represented in the eastern cordillera of Colombia (which includes Tobia and Villeta) by the spe-
cies 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.

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Mycobacterium bovis
BCG–Associated Osteomyelitis/Osteitis, Taiwan

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To the Editor: Thirty-eight patients with Mycobacterium bovis BCG–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 species of the Mycobacterium tuberculosis complex, using a kit for the Tokyo-172 vaccine strain spoligotyping, was established in 2004 (1). Since 2008, the isolated extrapulmonary tuberculosis strains and pathologic specimens collected from children <5 years of age have been sent to the national reference 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, children’s hospital information was stored in the Taiwan Centers for Disease Control database and used for research.

Of the 38 compensated BCG osteomyelitis/osteitis patients, 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 inoculation was 16.2 ± 16.6 days. Symptoms or signs began 3–32 months (average 12.4 ± 6.1 months) after BCG vaccination; for 68%, symptoms or signs developed 7–18 months after vaccination (online Technical Appendix Figure, http://wwwnc.cdc.gov/EID/article/21/3/14-0789-Techapp1.pdf). 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 upper 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 involved: 5 sternums, 2 thoracic vertebrae, and 1 right rib. Presentation included a mass (25 [66%] children), tender- ness (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 markers or to chest radiographs, except for 1 child with rib

Figure. Number of patient applications for compensation as a result of Mycobacterium bovis BCG osteomyelitis/osteitis to vaccine injury compensation program, Taiwan, 1998–2012.
**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.