
Address for correspondence: Keun Hwa Lee, Department of Microbiology and Immunology, Jeju National University College of Medicine, 15, Aran 13-gil, Jeju 63241, South Korea; email: yomust7@jejunu.ac.kr

**Spotted Fever Group Rickettsiae in Inner Mongolia, China, 2015–2016**

Gaowa, Wulantuya, Xuhong Yin, Shengchun Guo, Chunlian Ding, Minzhi Cao, Hiroki Kawabata, Kozue Sato, Shuji Ando, Hiromi Fujita, Fumihiko Kawamori, Hongru Su, Masahiko Shimada, Yuko Shimamura, Shuichi Masuda, Norio Ohashi

Author affiliations: College of Hetao, Bayan Nur City, Inner Mongolia, China (Gaowa, Wulantuya, X. Yin, S. Guo, C. Ding); Bayan Nur Centers for Disease Control and Prevention, Bayan Nur City (M. Cao); National Institute of Infectious Diseases, Shinjuku-ku, Tokyo, Japan (H. Kawabata, K. Sato, S. Ando); Mahara Institute of Medical Acarology, Anan City, Tokushima, Japan (H. Fujita); University of Shizuoka, Shizuoka City, Japan (F. Kawamori, H. Su, M. Shimada, Y. Shimamura, S. Masuda, N. Ohashi)

DOI: https://doi.org/10.3201/eid2411.162094

We found *Rickettsia raoultii* infection in 6/261 brucellosis-negative patients with fever of unknown origin in brucellosis-endemic Inner Mongolia, China. We further identified *Hyalomma asiaticum* ticks associated with *R. raoultii*, *H. marginatum* ticks associated with *R. aeschlimannii*, and *Dermacentor nuttalli* ticks associated with both rickettsiae species in the autonomous region.

S**potted** fever group rickettsiae (SFGR) are vector-borne pathogens. In China, 5 SFGR genotypes have been identified as causative agents of human rickettsiosis: *R. heilongjiangensis*, *R. sibirica* subsp. *sibirica* BJ-90, *Candidatus* Rickettsia tarasевичiae, *R. raoultii*, and *Rickettsia* sp. XY99 (1–4).

Brucellosis, a zoonotic disease, is highly endemic to Inner Mongolia, China, and is increasing in workers in agriculture or animal husbandry (5). However, some agriculture workers with brucellosis-like symptoms, including general malaise and fever, were seronegative for *Brucella* spp. We suspected that fever of unknown origin among brucellosis-seronegative patients might be caused by tick-borne pathogens. We identified 6 cases of human *R. raoultii* infections in brucellosis-seronegative patients in western Inner Mongolia, and we investigated exposure to ticks infected with SFGR.

During 2015–2016, we obtained 261 blood samples from brucellosis-seronegative patients with fever of unknown origin in Bayan Nur Centers for Disease Control and Prevention (Bayan Nur City, Inner Mongolia, China). The review board of the Department of Medicine at College of Hetao (Bayan Nur City) approved the study. We extracted DNA from each blood sample using the DNeasy Mini Kit (QIAGEN, Hilden, Germany) and conducted PCR targeting SFGR *gltA* (6). The PCR primers used, *gltA*-Fc (5′-CGAAGTCCCGGTATTAGAATG-3′) and *gltA*-Rc (5′-CTTGAAGAGCCGAGCTTCAAG-3′), were described previously (4). We designed the primers 16S rDNA R-2F (5′-GAAGATTCTTCTTCTCGGTTFCCGC-3′), 16S rDNA R-2R (5′-GTCCTGCTTCCCTCTGTAAAC-3′), rompA-Fb (5′-GGTGCGAATATAGACCCTGA-3′), and rompA-Ra (5′-CTTAGCTAGGACCTGACCA-3′) for this study and deposited the sequences obtained of *gltA*, *ompA*, and 16S rDNA into GenBank (accession nos. MH267733–47). We used genomic DNA extracted from L929 cells infected with *Rickettsia* sp. LON-13 (gltA: AB516964) as a positive control.

We detected *gltA* amplicons from 6/261 (2.3%) blood samples (Table). All 6 patients had strong malaise and mild fever of 36.8°C–37.3°C but no rash. Five of these patients also had arthralgia and vomiting.

Sequence and phylogenetic analysis showed that the sequences of 6 nearly full-length (1.1 kb) *gltA* amplicons with were identical to each other and to *R. raoultii* *gltA* (GenBank accession no. DQ365803). We further analyzed *ompA* and 16S rDNA in *gltA*-positive samples. All 6 samples were PCR positive for both genes; 552-bp sequences of the amplicons were identical to each other and to *R. raoultii* *ompA* (GenBank accession no. AH015610), and 389-bp sequences of the amplicons were identical to sequences of *R. raoultii* 16S rDNA (GenBank accession no. EU036982). PCR results were negative for the genes *Anaplasma phagocytophilum* p44/omp2, *Ehrlichia chaffeensis* p28/omp-1, and *Borrelia* spp. flaB. An indirect immunofluorescence assay showed that IgM and IgG titers against *R. japonica* were 40–80 for IgM in 3 patients and 160 for IgG in 2 patients.
To assess patients’ risk of infection with SFGR by tick exposure, we collected 2,458 ticks morphologically identified as *Hyalomma asiaticum* (n = 766), *Dermacentor nuttalli* (n = 1,418), and *Rhipicephalus turanicus* (n = 76) from livestock and pet animals including sheep, cattle, camels, and dogs in western Inner Mongolia during 2015–2016 (online Technical Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/24/11/16-2094-Techapp1.pdf). We collected unattached ticks within animal hair, but not attached ticks. We prepared DNA extracted from salivary glands of each tick and conducted PCR screening by rickettsial detection as described. We detected gltA in 1,266 (51.5%) of the total 2,458 ticks.

We classified the amplicons into 2 groups by restriction fragment-length polymorphism using *Alu* and *Rsa*I, and we sequenced 25–45 representative amplicons in each group. On the basis of this analysis, we found that the sequences from the 2 groups were either identical to that of *R. raoultii* (GenBank accession no. DQ365803) or to that of *R. aeschlimannii* (GenBank accession no. HM050276) (Table; online Technical Appendix Figure 2). We detected *R. raoultii* DNA in *H. asiaticum* (118/766, 15.4%) and *D. nuttalli* (830/1,418, 58.5%) ticks and *R. aeschlimannii* DNA from *H. marginatum* (160/198, 80.8%) and *D. nuttalli* (158/1,418, 11.1%) ticks. We did not detect rickettsial DNA in *R. turanicus* ticks (0/76, 0%).

Recently, human cases of *R. raoultii* infection have been reported in China, including northeastern Inner Mongolia (1,4). Potential vectors for *R. raoultii* are *Dermacentor* spp. ticks in Europe, Turkey, and northern Asia and *Haemaphysalis* spp. and *Amblyomma* sp. ticks in southern Asia (7,8). Other studies have identified *Hyalomma* spp., *Rhipicephalus* spp., and *Amblyomma* sp. ticks as potential vectors for *R. aeschlimannii* (7,8); human cases of *R. aeschlimannii* infection have been reported in Italy and Morocco (7,9). We detected *R. raoultii* in *H. asiaticum* as well as *D. nuttalli* ticks, but in Mongolia, *R. raoultii* has been detected only in *D. nuttalli* ticks, and not *H. asiaticum* ticks (10). We identified *D. nuttalli* ticks as another potential vector for *R. aeschlimannii*. Our work contributes to the knowledge of the epidemiology, clinical characteristics, and known tick vectors associated with *R. raoultii* and *R. aeschlimannii*.

**Acknowledgments**

We thank Asaka Ikegaya for providing *Rickettsia japonica* antigen slides.

This work was supported by grants from the National Natural Science Foundation of China (nos. 31660032 and 31660044); Natural Science Foundation of Inner Mongolia (2015BS0331); Bayan Nur Science and Technology Project from Bayan Nur Bureau for Science and Technology; Inner Mongolia Higher Education Science and Technology Project (NJJY2016C01); and Startup Fund for Talented Scholar in College of Hetao (to Gaowa). The research was partially supported by the Research Program on Emerging and Re-emerging Infectious Diseases from Japan Agency for Medical Research and Development (AMED) to N.O., H.K., and S.A.

**About the Author**

Dr. Gaowa is an associate professor in Inner Mongolia Key Laboratory of Tick-Borne Zoonosis, Department of Medicine, College of Hetao, Bayan Nur, Inner Mongolia, China. Her primary research interests are molecular biology, ecology, and epidemiology of zoonotic parasites, especially tickborne pathogens.

**References**


---

**Table. PCR survey of SFGR infections in patients and ticks, Inner Mongolia, China, 2015–2016**

<table>
<thead>
<tr>
<th>Patient type or tick species</th>
<th>No. tested</th>
<th><em>R. raoultii</em></th>
<th><em>R. aeschlimannii</em></th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brucellosis-seronegative patients</td>
<td>261</td>
<td>6 (2.3)</td>
<td>0</td>
<td>6 (2.3)</td>
</tr>
<tr>
<td>Ticks</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Hyalomma asiaticum</em></td>
<td>766</td>
<td>118 (15.4)</td>
<td>0</td>
<td>118 (15.4)</td>
</tr>
<tr>
<td><em>Hyalomma marginatum</em></td>
<td>198</td>
<td>0</td>
<td>160 (80.8)</td>
<td>160 (80.8)</td>
</tr>
<tr>
<td><em>Dermacentor nuttalli</em></td>
<td>1,418</td>
<td>830 (58.5)</td>
<td>158 (11.1)</td>
<td>988 (68.7)</td>
</tr>
<tr>
<td><em>Rhipicephalus turanicus</em></td>
<td>76</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Total ticks</td>
<td>2,458</td>
<td>948 (38.6)</td>
<td>318 (12.9)</td>
<td>1,266 (51.5)</td>
</tr>
</tbody>
</table>

*SFGR, spotted fever group rickettsiae.
†We did not detect dual infection with *R. raoultii* and *R. aeschlimannii* in *D. nuttalli* ticks in this study.*
Japanese Spotted Fever in Eastern China, 2013

Jiabin Li,† Wen Hu,† Ting Wu, Hong-Bin Li, Wanfu Hu, Yong Sun, Zhen Chen, Yonglin Shi, Jia Zong, Adams Latif, Linding Wang, Li Yu, Xue-Jie Yu, Bo-Yu Liu, Yan Liu

Author affiliations: The First Affiliated Hospital of Anhui Medical University, Hefei, China (J. Li, T. Wu, H.-B. Li); The First Affiliated Hospital of the University of Science and Technology of China, Hefei (Wen Hu); Anhui Center for Disease Control and Prevention, Hefei (Wanfu Hu, Y. Sun, Y. Shi); Anhui Medical University, Hefei (Z. Chen, J. Zong, A. Latif, L. Wang, L. Yu, B.-Y. Liu, Y. Liu); Wuhan University School of Health Sciences, Wuhan, China (X.-J. Yu)

DOI: https://doi.org/10.3201/eid2411.170264

We isolated Rickettsia japonica from a febrile patient in Lu’an City, China, in 2013. Subsequently, we found an R. japonica seroprevalence of 54.8% (494/902) in the rural population of Anhui Province and an R. japonica prevalence in Haemaphysalis longicornis ticks of 0.5% (5/935). R. japonica and its tick vector exist in China.

†These authors contributed equally to this article.