Acknowledgments

We thank the following persons and institutions for their assistance in obtaining and identifying specimens: Amy Hancock-Ronemus, Paul Mead, Ted Nuttall, Brigette Husband, and Kerry Pollard; the Department of Parasitology, College of Veterinary Medicine, University of Pennsylvania; the Schuylkill Wildlife Rehabilitation Center; and the Philadelphia Department of Public Health.

Julie R. Sinclair, Alisa Newton, Keith Hinshaw, George Fraser, Patrina Ross, Esther Chernak, Caroline Johnson, and Nancy Warren

Author affiliations: Centers for Disease Control and Prevention, Atlanta, Georgia, USA (J.R. Sinclair); Philadelphia Zoo, Philadelphia, Pennsylvania, USA (A. Newton, K. Hinshaw); Pennsylvania Bureau of Laboratories, Lionville, Pennsylvania, USA (G. Fraser, N. Warren); and Philadelphia Department of Public Health, Philadelphia (P. Ross, E. Chernak, C. Johnson)

DOI: 10.3201/eid1409.071690

References


Address for correspondence: Julie R. Sinclair, CDC Quarantine Station–Philadelphia, P.O. Box 144, Essington, PA 19029, USA; email: bwg5@cdc.gov

---

Genotyping of Orientia tsutsugamushi from Humans with Scrub Typhus, Laos

To the Editor: Rickettsial diseases have been only recently identified as underrecognized but important causes of fever of unknown origin in Laos. In 2006, 63 (14.8%) of 427 adults with negative blood cultures admitted to Mahosot Hospital in Vientiane had scrub typhus, an infection caused by Orientia tsutsugamushi and transmitted by the bite of larval trombiculid mites (1). O. tsutsugamushi is characterized by a wide antigenic diversity, and isolates are conventionally classified on the basis of reactivity with hyperimmune serum against prototype strains (e.g., Karp, Kato, Gilliam, Kawasaki, Kuroki, or Shimosogi). The 4 hypervariable regions within the 56-kDa type-specific antigen of O. tsutsugamushi, which is located on the outer membrane surface, are considered to play an essential role in type strain assignment (2).

In the Laos study (1), in addition to acute-phase serum samples, a 5-mL blood sample anticoagulated with EDTA was collected at admission from all patients. After centrifugation, buffy coat of the serum sample was removed and stored at –80°C (1). DNA was extracted from buffy coat samples of 63 patients whose conditions were diagnosed by immunofluorescence assay as scrub typhus (3). Two amplification reactions were performed, a real-time quantitative PCR with a probe targeting the O. tsutsugamushi 47-kDa outer membrane protein gene with appropriate primers and probes (4) and a standard PCR targeting a 372-nt fragment of the 56-kDa protein gene (3).

Buffy coat samples from 11 (17.5%) patients were positive for O. tsutsugamushi in the real-time quantitative PCR and 56-kDa antigen gene PCR (Table). All 11 patients were from Vientiane or Vientiane Province. PCR products for the 56-kDa gene fragments were purified and sequenced as described (3). Comparison (3,5) of amplicons for the 11 patients with each other and with GenBank sequences identified 6 genotypes. Percentages of nucleotide sequence similarity with other sequences available in GenBank ranged from 95.9% to 100% (Table). Interpretation of our results was also supported by recent phylogenetic studies that compared sequences of the entire 56-kDa type-specific antigen gene of isolates from Thailand (6). LaoUF238 and LaoUF220 genotypes clustered with those of strains related to the Karp serotype, and LaoUF136 and LaoUF187 clustered with genotypes of strains related to the Gilliam serotype (2). Other genotypes found in this study were grouped in 2 clusters that contained genotypes identified in Thailand (5) and Taiwan (7) that have not been linked to a reference serotype (Table).

Detection of O. tsutsugamushi in humans in Laos provides useful information on genotypes prevalent in this country. Our results were confirmed by using 2 target genes in 2 PCRs. No differences were found between the number of days of fever in 11 PCR-positive patients and number of days of fever in 52 PCR-negative patients. However, the PCR-negative patients may not have had bacteremia at the time of sample collection.

Diversity of O. tsutsugamushi genotypes found in Laos includes...
genotypes closely related to genotypes from Thailand and Taiwan. This diversity raises doubt about usual concepts because it has been thought that *O. tsutsugamushi* genotypes are restricted to specific geographic areas and to specific mite vectors (8). Furthermore, these results might have clinical repercussions because sequence variations within the 56-kDa protein gene correlate with antigenic diversity of genotypes of *O. tsutsugamushi*. This finding is supported by data for sequences of the entire 56-kDa gene of different isolates (6) and for monoclonal and human and animal polyclonal antibodies used to map antigenic differences among isolates with known sequence variations (9).

Although our data are preliminary, diversity of nucleotide sequences of the 56-kDa protein–encoding gene in isolates from Laos might limit sensitivity and specificity of serologic methods. A recent study showed that addition of a serotype to the panel of *O. tsutsugamushi* antigens used for testing improved sensitivity of antibody detection in patients in Thailand (10). We demonstrated that, in analysis of sera in the diagnosis of scrub typhus contracted in Laos, antigen pools should contain at least Karp and Gilliam strain antigens. Furthermore, new genotypes identified in patients in Laos might be related to previously unrecognized type strains. However, cross-reactivity with Gilliam, Kato, and Kawasaki serotypes enabled serologic diagnosis in the initial study, including 1 patient infected with a Karp-related bacteria (1).

Phylogenetic studies based on larger fragments of sequences of the 56-kDa protein–encoding gene and of other genes of *O. tsutsugamushi* would help to better characterize the new genotypes identified in our study and their relationship with known serotypes. Expanding the panel of antigens used to test patients suspected of having scrub typhus to take into account local antigenic diversity would improve sensitivity of serologic assays for this disease.

**Acknowledgments**

We thank Khalid El Karkouri for help with phylogenetic studies; the patients, Vimone Soukkhaseum, Khamphong Phisasaka, Surn Soukkhaseum, KhampHAV, Vang Chu, Valy Keolouangkhot, Bertrand Martinez-Aussel, Ko Chang, Chirapha Darasavath, Oudayone Rattanavong, Siho Sisouphone, Mayfong Mayxay, Sisouphone Vidamaly,
Mayboun Heuangvongsy, Chanpheng Thammavong, Bouanhun Rasachack, Bounkhong Syhavong, Nicholas J. White, Suriyasak Thongpraseth, Anisone Changthongthip, Viengmone Davong, Olay Lattana, Manivanh Vongsouthav, Kai-ampong Keopaseuth, Sengmani Symanivong, Viengmula Sihalath, and Alatsany Chandara for participating in the study; and Ponmek Dalaloy and Sommone Phounsavath for support.

This study was supported by the Wellcome Trust–Mahosot Hospital–Oxford Tropical Medicine Research Collaboration, which was supported by the Wellcome Trust of Great Britain.

Philippe Parola, Stuart D. Blacksell, Rattanaphone Phetsouvanh, Simaly Phongmany, Jean-Marc Rolain, Nicholas P.J. Day, Paul N. Newton, and Didier Raoult

Author affiliations: World Health Organization Collaborative Center for Rickettsial Diseases and Other Arthropod Borne Bacterial Diseases, Marseille, France (P. Parola, J.-M. Rolain, D. Raoult); Mahosot Hospital, Vientiane, Laos (S.D. Blacksell, R. Phetsouvanh, S. Phongmany, N.P.J. Day, P.N. Newton); University of Oxford, Oxford, United Kingdom (S.D. Blacksell, N.P.J. Day, P.N. Newton); and Mahidol University, Bangkok, Thailand (S.D. Blacksell, N.P.J. Day)

DOI: 10.3201/eid1409.071259

References

genetic characterization of Orientia tsutsu
sakorn S, et al. Causes of acute, undifferentiated, febrile illness in rural Thailand: re
sults of a prospective observational study. Ann Trop Med Parasitol. 2006;100:363–70. DOI: 10.1179/136485906X112158

Address for correspondence: Didier Raoult, Unité des Rickettsies, Centre National de la Recherche Scientifique–Institut de Recherche pour le Développement, Unité Mixte de Recherche 6236, World Health Organization Collaborative Center for Rickettsioses and Other Arthropod Borne Bacterial Diseases, Faculté de Médecine, 27 Bd Jean Moulin, 13005 Marseille, France; email: didier.raoult@gmail.com

The opinions expressed by authors contributing to this journal do not necessar
ily reflect the opinions of the Centers for Disease Control and Prevention or the institutions with which the authors are af
filiated.

Clindamycin-Resistant Clone of Clostridium difficile PCR Ribotype 027, Europe

To the Editor: Since 2003, outbreaks of Clostridium difficile–associated disease (CDAD) associated with the emergence of a hypervirulent strain have been reported worldwide (1,2). www.eurosurveillance.org/em/v12n06/1206-221.asp). This strain has been associated with increased disease severity and attributable mortality. Patients infected with C. difficile 027 fail to respond to metronidazole therapy (1). Several typing methods have been applied to further characterize C. difficile PCR ribotype-027, including pulsed-field gel electrophoresis (PFGE) (North American pulsed field type 1) and restriction enzyme analysis (REA) (BI). PFGE and REA are widely used in the United States; PCR ribotyping is more commonly used throughout Europe. More recently, 2 multiple-locus variable-number tandem-repeat analysis (MLVA) protocols have been applied to type C. difficile, and these proved more discriminatory compared to other methods (3,4). Furthermore, MLVA can subgroup geographically diverse 027 isolates (G. Killgore et al., unpublished data) as well as 027 isolates that are common to 1 institution (5).

We reported a case of C. difficile PCR 027 in Ireland, where the isolate had an identical antibiotic profile compared with those strains reported across Europe (6,7) (i.e., resistant to fluoroquinolones and erythromycin, susceptible to clindamycin). We have subsequently identified C. difficile 027 in 6 more healthcare settings. To date >100 Irish C. difficile 027 isolates have been characterized by analysis of their antibiogram profiles, toxinotyping, and 16S-23S rDNA PCR ribotyping. All C. difficile 027 isolates were resistant to moxifloxacin, gatifloxacin,