2.6%, and 1.4%, respectively, of the diagnosed CL cases (8). This trend could be due either to an increase of *L. braziliensis* prevalence in the forests of Guiana or to a greater presence of humans (e.g., military personnel, scientists, and tourists) in deep forest areas with hot spots of transmission. Favorable environmental conditions in a well-delimited zoonotic microfocus hot spot might have contributed to this high rate of transmission. However the relative genetic diversity of strains we observed among the 5 analyzed patients was unexpected, given the relatively small spatial and temporal scale of the transmission area, and indicates that the reservoirs in this restricted area were infested by distinct genotypes. Development of a peridomestic cycle, perhaps with specific reservoirs (pets) and vectors, cannot be excluded in the Saül area.

This case series suggests that caution should be taken in the diagnosis and treatment of CL in patients returning from the Amazonian rainforest, and a species-specific approach based on molecular identification should be proposed to provide appropriate medical management (9). Indeed, although *L. braziliensis* parasites cause <10% of CL acquired in French Guiana, this species is noteworthy for its involvement of the mucous membranes of the lips, nose, soft palate, or larynx. Also, *L. braziliensis* parasites usually fail to respond to pentamidine isethionate, the first-line treatment of *L. guyanensis* CL in French Guiana; instead, treatment of *L. braziliensis* infection relies on parenteral meglumine antimoniate or liposomal amphotericin B (f).

In summary, the geographic extension of and numeric increase in *L. braziliensis* cases in the Guiana ecoregion complex, as observed in the rest of South America, are worrisome, and continuous epidemiologic surveillance is needed. Infection with *L. braziliensis*, which is emerging and has potential to disseminate, must be considered in cases of CL acquired in this region. These issues have key implications for leishmaniasis treatment, which should be directed to the identified species (10).

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**References**

1. Schwartz E, Hatz C, Blum J. New World cutaneous leishmaniasis in travellers. Lancet Infect Dis. 2006;6:342–9. http://dx.doi.org/10.1016/S1473-3099(06)70492-3
2. Desjeux P, Dedet JP. Isoenzyme characterization of 112 Leishmania isolates from French Guiana. Trans R Soc Trop Med Hyg. 1989;83:610–2. http://dx.doi.org/10.1016/0035-9203(89)90373-8
3. El Baidouri F, Diancourt L, Berry V, Chevenet F, Pratlong F, Marty P, et al. Genetic structure and evolution of the Leishmania genus in Africa and Eurasia: what does MLSA tell us. PLoS Negl Trop Dis. 2013;7:e2255. http://dx.doi.org/10.1371/journal.pntd.0002255
4. Huson DH, Bryant D. Application of phylogenetic networks in evolutionary studies. Mol Biol Evol. 2006;23:254–67. http://dx.doi.org/10.1093/molbev/msj030
5. Krolewiecki AJ, Gil JW, Quipildor M, Cajal SP, Pravia C, Juarez M, et al. Restricted outbreak of American cutaneous leishmaniasis with high microfocal transmission. Am J Trop Med Hyg. 2013;88:578–82. http://dx.doi.org/10.4269/ajtmh.12-0475
6. Andrade MS, Brito ME, Silva ST, Ishikawa E, Carvalho SM, Brandao-Filho SP. New outbreak of American cutaneous leishmaniasis in a military training center in the Zona da Mata region, in the north of the State of Pernambuco [in Portuguese]. Rev Soc Bras Med Trop. 2009;42:594–6. http://dx.doi.org/10.1590/S0037-86822009000500022
7. Sanchez JL, Diniegia BM, Small JW, Miller RN, Andujar JM, Weina PJ, et al. Epidemiologic investigation of an outbreak of cutaneous leishmaniasis in a defined geographic focus of transmission. Am J Trop Med Hyg. 1992;47:47–54.
8. Carme B, Simon S, Coupie P. Epidemiologic survey of leishmaniasis in French Guiana. In: Proceedings of the 3rd French Indies and Guiana Interregional Meeting; 2012 Oct 26–27. Saint-Maurice (France): Institut National de Veille Sanitaire; 2012.
9. Lavergne RA, Iriart X, Martin-Blondel G, Chauvin P, Menard S, Fillaux J, et al. Contribution of molecular diagnosis to the management of cutaneous leishmaniasis in travellers. Clin Microbiol Infect. 2014;20:OS28–30.
10. Hodiamont CJ, Kager PA, Bart A, de Vries HJ, van Thiel PP, Leenstra T, et al. Species-directed therapy for leishmaniasis in returning travellers: a comprehensive guide. PLoS Negl Trop Dis. 2014;8:e2832. http://dx.doi.org/10.1371/journal.pntd.0002832

Address for correspondence: Antoine Berry, Department of Parasitology, Toulouse University Hospital, Place du Docteur Baylac TSA 40031, 31059 Toulouse CEDEX 9, France; email: berry.a@chu-toulouse.fr

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**Ciprofloxacin-Resistant *Shigella sonnei* Associated with Travel to India**

Niall De Lappe, Jean O’Connor, Patricia Garvey, Paul McKeown, Martin Cormican

Author affiliations: University Hospital Galway, Galway, Ireland (N. De Lappe, J. O’Connor, M. Cormican); Health Protection Surveillance Centre, Dublin, Ireland (P. Garvey, P. McKeown)

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To the Editor: Shigellosis is an uncommon infection in many industrialized countries, and many cases are linked to travel to *Shigella* spp.–endemic countries. The epidemiology of *Shigella* infections in developing countries is changing. *S. sonnei* seems to be replacing the more antigenically diverse *S. flexneri* in regions undergoing economic development and improvements in water quality (1).

In 2012, a total of 29 cases of shigellosis were reported in Ireland through the Computerized Infectious Disease Reporting system (crude incidence rate 0.63 cases/100,000 population). Isolates from 20 (69%) of those 29 cases were submitted to the National Reference Laboratory in Galway, Ireland, for additional typing. In 2013, a total of 43 isolates...
were submitted for typing, more than double the 20 isolates submitted for 2012. This increase may be associated with a change in diagnostic methods: the increasing use of molecular methods for primary testing (2). During 2010–2013, the most common isolates were S. sonnei (54%) and S. flexneri (38%).

Isolate identification was confirmed by using VITEK 2 (bioMérieux, Marcy l’Etoile, France) and serotyping performed by using slide agglutination with commercial antisera (Sifin, Dusseldorf, Germany, and Mast, Liverpool, UK). Antimicrobial drug susceptibility testing was performed with disk-diffusion tests or Etests (2000–2009) and by broth microdilution (2010–2013) (Sensititre, Trek Diagnostic Systems, Cleveland, OH, USA). Susceptibility to ampicillin, chloramphenicol, streptomycin, sulfamethoxazole, tetracycline, trimethoprim, naladixic acid, ciprofloxacin, gentamicin, cefazidime, cefpodoxime, and cefotaxime was assessed by using criteria from the European Committee on Antimicrobial Susceptibility Testing (http://www.eucast.org/clinical_breakpoints). Since October 2013, testing has also included azithromycin, tigecycline, meropenem, and cefepime. Pulsed-field gel electrophoresis (PFGE) was performed on all S. sonnei isolates by using the PulseNet method developed by the Centers for Disease Control and Prevention (3). Fisher exact test was applied to assess the significance of the association of ciprofloxacin resistance with reported travel to the subcontinent of India.

Although infection with S. sonnei is generally self-limiting, antimicrobial drug therapy is necessary for some patients and may reduce duration of shedding in feces (4). Ciprofloxacin is widely recommended for use in the absence of susceptibility test results. Alternative agents for therapy include ceftriaxone and azithromycin.

For 2000–2009, none of the 65 S. sonnei isolates submitted for typing were resistant to ciprofloxacin. For 2010–2013, the number of ciprofloxacin-resistant S. sonnei isolates and the total number of S. sonnei isolates submitted for testing were 6/17 (2010), 2/20 (2011), 4/12 (2012), and 12/23 (2013). All 24 ciprofloxacin-resistant isolates were co-resistant to trimethoprim, and all but 2 were also resistant to streptomycin, sulfamethoxazole, and tetracycline. Cefotaxime resistance in 1 isolate was associated with extended-spectrum β-lactamase production. Azithromycin resistance has not been detected since testing for this resistance began in October 2013.

All 24 isolates had indistinguishable or closely related (>92%) XbaI-PFGE profiles (Figure). The XbaI cluster also included 21 of 50 ciprofloxacin-susceptible S. sonnei isolates submitted during 2000–2013. Use of a second enzyme (BlnI) on a subset of the 24 isolates confirmed the close relationship among these 24 isolates (data not shown).

Data from the Computerized Infectious Disease Reporting system (2010–2013) identified 72 reported cases of S. sonnei infection, of which 24 were ciprofloxacin resistant. Of 15 isolates associated with travel to the subcontinent of India, 11 were ciprofloxacin resistant, but of 47 other isolates for which the country of infection was reported, only 9 were ciprofloxacin resistant, a significant difference (p<0.0001).

**Figure.** Dendrogram of ciprofloxacin-resistant Shigella sonnei digested with XbaI enzyme. Isolate identification numbers and country location for origin of infection are shown. In column on far right, antibiogram abbreviations indicate resistance to antimicrobial drugs: A, ampicillin; S, streptomycin; Su, sulfamethoxazole; T, tetracycline; Tm, trimethoprim; Na, nalidixic acid; Cp, ciprofloxacin; Ctx, cefotaxime. Scale bar indicates evolutionary distance. PFGE, pulsed-field gel electrophoresis.
International concern is growing regarding antimicrobial drug resistance in *Shigella* infections associated with India. Fluoroquinolone resistance emerged in *S. dysenteriae* in 2002, in *S. flexneri* in 2004, and in *S. sonnei* in 2007 (5). Studies from Japan have also reported an association between travel to India and infection with an *S. sonnei* clonal group that was multidrug resistant, including resistance to nalidixic acid (6). Furthermore, ciprofloxacin-resistant *S. sonnei* isolates from foodborne outbreaks in India in 2009 and 2010 (7) had *XbaI*-PFGE types and resistance profiles visually indistinguishable from those reported in our study. A study of *S. sonnei* isolates in Bhutan showed that this clonal group was also common there (8). Furthermore, a 2010 outbreak of ciprofloxacin-resistant *S. sonnei* in Canada associated with men who have sex with men showed *XbaI* and *BlnI*-PFGE patterns that appear similar to the patterns for isolates in this study (9).

Antimicrobial drug resistance is a major global problem that is likely to be exacerbated in places with poor sanitation and intensive use of antimicrobial drugs in humans and animals. These factors have contributed to increased ciprofloxacin resistance in *Salmonella enterica* serovars Typhi and Paratyphi A (10).

A review of published literature and informal communication indicates that our observation of ciprofloxacin resistance in *S. sonnei* infections associated with travel to India is part of a general global trend. This increasing resistance suggests that ciprofloxacin may no longer be suitable for empiric therapy for *S. sonnei* infection, particularly for patients with a history of travel to the subcontinent of India.

References
1. Holt KE, Baker S, Weill FX, Holmes E, Kitchen A, Yu J, et al. *Shigella sonnei* genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. Nat Genet. 2012;44:1056–9. http://dx.doi.org/10.1038/ng.2369
2. DeLappe N, O’Connor J, Morris D, Cormican M. Molecular detection of *Shigella* species impacts on apparent epidemiology and reference laboratory workload. In: Final Program of the 24th European Congress of Clinical Microbiology and Infectious Diseases; Barcelona, Spain; 2014 May 10–13; ePoster 091. Basel (Switzerland): European Society of Clinical Microbiology and Infectious Diseases; 2014.
3. Ribot EM, Fair MA, Gautom R, Cameron DN, Hunter SB, Swaminathan B. Standardization of pulsed-field gel electrophoresis protocols for the subtyping of *Escherichia coli* O157:H7, *Salmonella* and *Shigella* for PulseNet. Foodborne Pathog Dis. 2006;3:59–67. http://dx.doi.org/10.1089/fpd.2006.3.59
4. World Health Organization. Guidelines for the control of shigellosis, including epidemics of *Shigella dysenteriae* type 1. 2005 [cited 2015 Mar 4]. http://whoqlibrary.who.int/publications/2005/9241592330.pdf
5. Nandy S, Mitra U, Rajendran K, Dutta P, Dutta S. Subtype prevalence, plasmid profiles and growing fluoroquinolone resistance in *Shigella* from Kolkata, India (2001–2007): a hospital-based study, Trop Med Int Health. 2010;15:499–507. http://dx.doi.org/10.1111/j.1365-3156.2010.02656.x
6. Izumiya H, Tada Y, Ito K, Morita-Ishihara T, Ohnishi M, Terajima J, et al. Characterization of *Shigella sonnei* isolates from travel-associated cases in Japan. J Med Microbiol. 2009;58:1486–91. http://dx.doi.org/10.1099/jmm.0.011809-0
7. Nandy S, Dutta S, Ghosh S, Ganai A, Jyothi R, Ramani Bai JT, et al. Foodborne-associated *Shigella sonnei*, India, 2009 and 2010. Emerg Infect Dis. 2011;17:2072–4. http://dx.doi.org/10.3201/eid1711.110403
8. Rueket S, Wangchuk S, Dorji T, Tshering KP, Pootong P, Nohthai P, et al. Molecular characterization and PCR-based replicon typing of multidrug resistant *Shigella sonnei* isolates from an outbreak in Thimphu, Bhutan. BMC Res Notes. 2014;7:95.
9. Gaudreau C, Ratnayake R, Pilon PA, Gagnon S, Roger M, Lèvesque S. Ciprofloxacin-resistant *Shigella sonnei* among men who have sex with men, Canada, 2010. Emerg Infect Dis. 2011;17:1747–50. http://dx.doi.org/10.3201/eid1709.102034
10. Dutta S, Das S, Mitra U, Jain P, Roy I, Ganguly S, et al. Antimicrobial resistance, virulence profiles and molecular subtypes of *Salmonella enterica* serovars Typhi and Paratyphi A blood isolates from Kolkata, India during 2009–2013. PLoS ONE. 2014;9:e101347. http://dx.doi.org/10.1371/journal.pone.0101347

Address for correspondence: Niall De Lappe, National *Salmonella*, *Shigella* and *Listeria* Reference Laboratory, Department of Medical Microbiology, University Hospital Galway, Galway, Ireland; email: niall.delappe@hsc.ie

Fatal *Balamuthia mandrillaris* Meningoencephalitis in the Netherlands after Travel to The Gambia

Nadine A.M.E. van der Beek,¹ Carla van Tienen,¹ Jubi E. de Haan, Jeroen Roelfsema, Pieter J. Wismans, Perry J.J. van Genderen, Herve L. Tanghe, Rob M. Verdijk, Maarten J. Titulaer,² Jaap J. van Hellemond²

Author affiliations: Erasmus University Medical Centre, Rotterdam, the Netherlands (N.A.M.E. van der Beek, C. van Tienen, J.E. de Haan, H.L. Tanghe, R.M. Verdijk, M.J. Titulaer, J.J. van Hellemond); National Institute for Public Health and the Environment, Bilthoven, the Netherlands (J. Roelfsema); Harbor Hospital, Rotterdam (P.J. Wismans, P.J.J. van Genderen, J.J. van Hellemond)

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To the Editor: *Balamuthia mandrillaris* is a free-living ameba that has a worldwide distribution in soil and was first reported in 1990 (1). Approximately 200 *B. mandrillaris* meningoencephalitis cases have been described, mostly from warm climate areas in South America. Its prevalence in the United States is estimated to be 1 case/year (2). However, *B. mandrillaris* meningoencephalitis

¹These first authors contributed equally to this article.
²These senior authors contributed equally to this article.